

Search completed: December 8, 2003, 09:55:35
Job time : 6.8 secs

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15-SEP-2003 (Rel. 42, Last annotation update)
Coagulation factor IX/factor X-binding protein B chain precursor
(IX/X-BP).
Trimeresurus flavoviridis (Habu).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
Viperidae; Crotalinae; Trimeresurus.
NCBI_TaxID=89087;
[1]
SEQUENCE FROM N.A.
MEDLINE=96184662; PubMed=8645314;
Matsuzaki R., Yoshihara E., Yamada M., Shima K., Atoda H., Morita T.;
"cDNA cloning of IX/X-BP, a heterogeneous two-chain anticoagulant
protein from snake venom.";
Biochem. Biophys. Res. Commun. 220:382-387 (1996).
[2]
SEQUENCE OF 24-146.
TISSUE=Venom;
RX MEDLINE=91332000; PubMed=1831197;
Atoda H., Hyuga M., Morita T.;
"The primary structure of coagulation factor IX/factor X-binding
protein isolated from the venom of Trimeresurus flavoviridis.
Homology with asialoglycoprotein receptors, proteoglycan core
protein, tetranectin, and lymphocyte Fc epsilon receptor for
immunoglobulin E.";
J. Biol. Chem. 266:14903-14911 (1991).
[3]
X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).
MEDLINE=9731317; PubMed=9187649;
Mizuno H., Fujimoto Z., Koizumi M., Kano H., Atoda H., Morita T.;
"Structure of coagulation factors IX/X-binding protein, a heterodimer
of C-type lectin domains.";
Nat. Struct. Biol. 4:438-441 (1997).
CC FACTOR X IN THE PRESENCE OF CALCIUM WHICH BINDS WITH FACTOR IX AND
CC -!- FUNCTION: ANTICOAGULANT PROTEIN WHICH BINDS WITH FACTOR IX AND
CC -!- FUNCTION: ANTICOAGULANT WITH A 1 TO 1 STOICHIOMETRY.
CC -!- SUBUNIT: HETERODIMER OF CHAINS A AND B LINKED BY A DISULFIDE BOND.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- MISCELLANEOUS: CALCIUM IS REQUIRED FOR LIGAND BINDING.
CC -!- SIMILARITY: Contains 1 C-type lectin family domain.

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or send an email to license@isb-sib.ch).

EMBL; D83332; BA011888.1; -
DR FIR; JC4691; JC4691.
DR PDB; 1LXX; 06-MAY-98.
DR PDB; 1BJ3; 16-AUG-99.
DR InterPro; IPR001304; Lectin C.
DR Pfam; PF00059; lectin c; 1.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS00615; C-TYPE LECTIN 1; 1.
DR PROSITE; PS00041; C-TYPE LECTIN 2; 1.
KW Lectin; Calcium; signal; 3D-structure.
FT SIGNAL 1 23
FT CHAIN 24 146
FT COAGULATION FACTOR IX/FACTOR X-BINDING
FT PROTEIN B CHAIN.
FT DOMAIN 24 144
FT C-TYPE LECTIN (LONG FORM).
FT DISULFID 25 36
FT BY SIMILARITY.
FT DISULFID 53 142
FT BY SIMILARITY.
FT DISULFID 98 98
FT INTERCHAIN (WITH C-102 OF A CHAIN).
FT DISULFID 119 134
FT BY SIMILARITY.
FT TURN 27 28
FT STRAND 30 32
FT TURN 33 34
FT STRAND 35 44
FT STRAND 46 54
FT HELIX 55 56
FT TURN 55 56
FT TURN 58 59

FT STRAND 61 62
FT HELIX 68 82
FT STRAND 86 88
FT TURN 94 97
FT STRAND 100 102
FT TURN 103 104
FT STRAND 113 113
FT STRAND 118 123
FT TURN 124 125
FT STRAND 126 133
FT TURN 134 135
FT STRAND 138 146
SQ SEQUENCE 146 AA; 16922 MW; 8E1961C59F96757C CRC64;
Query Match 78.2%; Score 133; DB 1; Length 146;
Best Local Similarity 72.4%; Pred. No. 1.1e-10;
Matches 21; Conservative 2; Mismatches 6; Indels 0; Gaps 0;
QY 1 DCSDWSSYEGHCYKVKFKQSKTWTDAESF 29
DB 24 DCPDSSSYEGHCYKVPSEPKNWADAENF 52
RESULT 3
ABA4 TRIAB STANDARD; PRT; 123 AA.
ID ABA4 TRIAB
AC P81114;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Alboaggregin A subunit 4.
OS Trimeresurus albobutris (White-lipped pit viper).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Crotalinae; Trimeresurus.
OX NCBI_TaxID=8765;
RN [1]
RP SEQUENCE.
RC TISSUE=Venom;
RX MEDLINE=98189535; PubMed=9531050;
RA Kowalska M.A., Tan L., Holt J.C., Peng M., Karczewski J.,
RA Calvete J.J., Niewiarowski S.;
RT "Alboaggregins A and B. Structure and interaction with human
platelets.";
RL Thromb. Haemost. 79:609-613 (1998).
CC -!- FUNCTION: Binds to platelet GPIb/IX receptor system and stimulates
CC -!- SUBUNIT: Heterotetramer of the subunits 1, 2, 3 and 4,
CC disulfide-linked.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Contains 1 C-type lectin family domain.
DR HSP; P23807; 1LXX.
DR InterPro; IPR002353; AntifreezeII.
DR InterPro; IPR001304; Lectin C.
DR Pfam; PF00059; lectin c; 1.
DR PRINTS; PR00356; ANTIFREEZEII.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS00615; C-TYPE LECTIN 1; 1.
DR PROSITE; PS00041; C-TYPE LECTIN 2; 1.
KW Lectin.
FT DOMAIN 1 121
FT C-TYPE LECTIN (LONG FORM).
FT DISULFID 2 13
FT BY SIMILARITY.
FT DISULFID 30 119
FT BY SIMILARITY.
FT DISULFID 96 111
FT BY SIMILARITY.
SQ SEQUENCE 123 AA; 14365 MW; D4CFBE1219C9B1E CRC64;
Query Match 77.1%; Score 131; DB 1; Length 123;
Best Local Similarity 69.0%; Pred. No. 1.7e-10;
Matches 20; Conservative 3; Mismatches 6; Indels 0; Gaps 0;
QY 1 DCSDWSSYEGHCYKVKFKQSKTWTDAESF 29
DB 1 DCPDSSSYEGHCYKVPSEPKNWADAENF 29

RESULT 4
 IXA TRIPL
 ID IXA TRIPL STANDARD; PRT; 152 AA.
 AC P23806; Q91246;
 DT 01-NOV-1991 (Rel. 20, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Coagulation factor IX/factor X-binding protein A chain precursor
 DE (IX/X-BP).
 OS Trimeresurus flavoviridis (Habu).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidodonta; Squamata; Scleroglossa; Serpentes; Colubroidea;
 OC Viperidae; Crotalinae; Trimeresurus.
 OX NCBI_TaxID=88087;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96184662; PubMed=8645314;
 RA Matsuzaki R., Yoshihara E., Yamada M., Shima K., Atoda H., Morita T.;
 RT "cDNA cloning of IX/X-BP, a heterogeneous two-chain anticoagulant
 protein from snake venom.";
 RL Biochem. Biophys. Res. Commun. 220:382-387(1996).
 RN [2]
 RP SEQUENCE OF 24-152.
 RC TISSUE=Venom;
 RX MEDLINE=91332000; PubMed=1831197;
 RA Atoda H., Hyuga M., Morita T.;
 RT "The primary structure of coagulation factor IX/factor X-binding
 protein isolated from the venom of Trimeresurus flavoviridis.
 RT Homology with asialoglycoprotein receptors, proteoglycan core
 protein, tetranectin, and lymphocyte Fc epsilon receptor for
 immunoglobulin E.";
 RL J. Biol. Chem. 266:14903-14911(1991).
 RN [3]
 RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).
 RX MEDLINE=97331317; PubMed=9187649;
 RA Mizuno H., Fujimoto Z., Koizumi M., Kano H., Atoda H., Morita T.;
 RT "Structure of coagulation factors IX/X-binding protein, a heterodimer
 of C-type lectin domains.";
 RL Nat. Struct. Biol. 4:438-441(1997).
 CC -1- FUNCTION: ANTICOAGULANT PROTEIN WHICH BINDS WITH FACTOR IX AND
 CC FACTOR X IN THE PRESENCE OF CALCIUM WITH A 1 TO 1 STOICHIOMETRY.
 CC -1- SUBUNIT: HETERODIMER OF CHAINS A AND B LINKED BY A DISULFIDE BOND.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- MISCELLANEOUS: CALCIUM IS REQUIRED FOR LIGAND BINDING.
 CC -1- SIMILARITY: Contains 1 C-type lectin family domain.
 CC
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 CC
 CC EMBL; D83331; BA011887.1; --
 CC PIR; JC4690; JC4690.
 CC PDB; 1LXX; 06-MAY-98.
 CC InterPro; IPR001304; Lectin_C.
 CC InterPro; IPR003990; Pancreatins_ac.
 CC Pfam; PF000059; lectin_c; 1.
 CC PRINTS; PR01504; PNCREATISAP.
 CC SMART; SM00034; CLECT; 1.
 CC PROSITE; PS00615; C_TYPE_LLECTIN_1; 1.
 CC PROSITE; PS00615; C_TYPE_LLECTIN_2; 1.
 CC PROSITE; PS00615; C_TYPE_LLECTIN_2; 1.
 KW Lectin; Calcium; Signal; 3D-structure.
 FT SIGNAL 1 23
 FT CHAIN 24 152 COAGULATION FACTOR IX/FACTOR X-BINDING
 FT
 FT DOMAIN 24 152 PROTEIN A CHAIN.
 FT DISULFID 24 152 C-TYPE LECTIN (LONG FORM).
 FT BY SIMILARITY.
 FT DISULFID 53 150 BY SIMILARITY.

FT DISULFID 102 102 INTERCHAIN (WITH C-98 OF B CHAIN).
 FT TURN 125 142 BY SIMILARITY.
 FT STRAND 27 28
 FT STRAND 30 31
 FT HELIX 36 44
 FT TURN 46 56
 FT STRAND 58 59
 FT HELIX 61 62
 FT STRAND 68 81
 FT STRAND 89 95
 FT STRAND 105 105
 FT TURN 107 108
 FT STRAND 111 111
 FT STRAND 117 117
 FT HELIX 119 121
 FT STRAND 125 128
 FT HELIX 130 132
 FT TURN 133 134
 FT STRAND 137 140
 FT TURN 142 143
 FT STRAND 146 152
 SQ SEQUENCE 152 AA; 17213 MW; FB3DDDD2369009263 CRC64;
 Query Match 72.4%; Score 123; DB 1; Length 152;
 Best Local Similarity 74.1%; Pred. No. 2.3e-09;
 Matches 20; Conservative 2; Mismatches 5; Indels 0; Gaps 0;
 QY 1 DCSDDSSSYEGHCYKVFQSKTWTDAE 27
 |||||
 DB 24 DCLSGSSSYEGHCYKAFKKTWEDAE 50
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 RESULT 5
 ABAL TRIAB
 ID ABAL TRIAB STANDARD; PRT; 131 AA.
 AC P8111;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Alboaggregin A subunit 1.
 OS Trimeresurus albobabris (White-lipped pit viper).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidodonta; Squamata; Scleroglossa; Serpentes; Colubroidea;
 OC Viperidae; Crotalinae; Trimeresurus.
 OX NCBI_TaxID=8765;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Venom;
 RX MEDLINE=98189535; PubMed=9531050;
 RA Kowalska M.A., Tan L., Holt J.C., Peng M., Karczewski J.,
 RA Calvete J.J., Niewiarowski S.;
 RT "Alboaggregins A and B. Structure and interaction with human
 RT platelets";
 RL Thromb. Haemost. 79:609-613(1998).
 CC -1- FUNCTION: Binds to platelet GPIb/IX receptor system and stimulates
 CC aggregation.
 CC -1- SUBUNIT: Heterotetramer of the subunits 1, 2, 3 and 4,
 CC disulfide-linked.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: Contains 1 C-type lectin family domain.
 DR HSSP; P23806; IIXX.
 DR InterPro; IPR001304; Lectin_C.
 DR Pfam; PF000059; lectin_c; 1.
 DR SMART; SM00034; CLECT; 1.
 DR PROSITE; PS00615; C_TYPE_LLECTIN_1; 1.
 DR PROSITE; PS00615; C_TYPE_LLECTIN_2; 1.
 KW Lectin.
 FT DOMAIN 1 129 C-TYPE LECTIN (LONG FORM).
 FT DISULFID 2 13 BY SIMILARITY.
 FT DISULFID 30 127 BY SIMILARITY.
 FT DISULFID 102 119 BY SIMILARITY.
 SQ SEQUENCE 131 AA; 15427 MW; B3569F5BF91F6624 CRC64;

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Query Match      70.8%; Score 120; DB 1; Length 131;
Best Local Similarity 65.5%; Pred.No. 4.9e-09;
Matches 19; Conservative 5; Mismatches 5; Indels 0; Gaps 0;
QY      1 DCSDDSSSYEGHCYKVFQSKTWTDAESF 29
Db      1 DCSFDSSSYDQYCYRVFKRIQTWEDAEFF 29

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ID	BOTB	BOTJA	STANDARD;	PRT;	125 AA.
DT	AC	P22030;			
DT	DT	01-AUG-1991 (Rel. 19, Created)			
DT	DT	01-JUL-1993 (Rel. 26, Last sequence update)			
DT	DT	15-SEP-2003 (Rel. 42, Last annotation update)			
DE	BT	botoctetin, beta chain (Platelet coagglutinin).			
OS	BT	Bothrops jararaca (Jararaca).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;				
OC	Viperidae; Crotalinae; Bothrops.				
OX	NCEI_TaxID=8724;				
RN	[1]				
RP	SEQUENCE AND DISULFIDE BONDS.				
RP	TISSUE=Venom;				
RC	MEDLINE=93157385; PubMed=8430107;				
RX	Usami Y., Fujimura Y., Suzuki M., Ozeki Y., Nishio K., Fukui H.,				
RA	Titani K.;				
RT	"Primary structure of two-chain botoctetin, a von Willebrand factor				
RT	modulator purified from the venom of Bothrops jararaca.";				
RL	Proc. Natl. Acad. Sci. U.S.A. 90:928-932(1993).				
RN	[2]				
RP	SEQUENCE OF 1-40.				
RC	TISSUE=venom;				
RX	MEDLINE=91129280; PubMed=1993206;				
RA	Fujimura Y., Titani K., Usami Y., Suzuki M., Oyama R., Matsui T.,				
RA	Fukuji H., Sugimoto M., Ruggeri Z.M.;				
RT	"Isolation and chemical characterization of two structurally and				
RT	functionally distinct forms of botoctetin, the platelet coagglutinin				
RT	isolated from the venom of Bothrops jararaca.";				
RL	Biochemistry 30:1957-1964(1991).				
RN	[3]				
RP	X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS).				
RC	MEDLINE=23118144; PubMed=12121649;				
RX	Fukuda K., Doggett T.A., Bankston L.A., Cruz M.A., Diacovo T.G.,				
RA	Liddington R.C.;				
RT	"Structural basis of von Willebrand factor activation by the snake				
RT	toxin botoctetin.";				
RL	Structure 10:943-950(2002).				
CC	-!- FUNCTION: Two-chain Botoctetin forms an activated complex with				
CC	vWF, and the complex then binds to platelet GPIb, resulting in				
CC	platelet agglutination.				
CC	-!- FUNCTION: There are two distinct forms of the von Willebrand.				
CC	factor-dependent platelet coagglutinin. The dimeric form is				
CC	34-times more active than the one-chain Botoctetin in promoting				
CC	vWF binding to platelets.				
CC	-!- SUBUNIT: Disulfide-linked dimer of an alpha and a beta chain.				
CC	vWF and Botoctetin form a soluble complex.				
CC	-!- SUBCELLULAR LOCATION: Secreted.				
CC	-!- SIMILARITY: Contains 1 C-type lectin family domain.				
DR	PIR; B47267; B47267.				
DR	PDB; 1IJK; 17-JUL-02.				
DR	PDB; 1LFVU; 14-FEB-01.				
DR	InterPro; IPR001304; Lectin_C.				
DR	Pfam; PF00059; lectin_c; 1.				
DR	SMART; SM00034; CLECT; 1.				
DR	PROSITE; PS00615; C TYPE LECTIN 1; FALSE_NEG.				
DR	PROSITE; PPS0041; C TYPE_LCTIN_2; 1.				
KW	Lectin; 3D-structure,				
FT	Disulfid 2 13				
FT	DISULFID 30 121				
FT	DISULFID 75 75				
FT	DISULFID 98 113				
FT					

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SQ  SEQUENCE  125 AA;  15037 MW;  1ED2027ED817FCA0 CRC64;
      70.0%;  Score 119;  DB 1;  Length 125;
Query Match  Best Local Similarity  65.5%;  Pred. No. 6.3e-09;
Matches 19;  Conservative  2;  Mismatches  8;  Indels  0;  Gaps  0;

Qy  1  DCSDDSSSYEGHCYKVKQSKTWTDAESF  29
Db  1  DCPDPDSSSYEGHCYKRFKQKWHMDAEF  29

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RESULT 7

BTOTA	BOTJA	STANDARD;	PRT;	133 AA.
ID	BOTA	BOTJA		
AC	P22029;			
DT	01-AUG-1991 (Rel. 19, Created)			
DT	01-JUL-1993 (Rel. 26, Last sequence update)			
DT	15-SEP-2003 (Rel. 42, Last annotation update)			
DE	Botrocetin, alpha chain (Platelet coagglutinin).			
OS	Bothrops jararaca (Jararaca).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;			
OC	Viperidae; Crotalinae; Bothrops.			
OX	NCBI_TaxID=8724;			
[1]				
RN	SEQUENCE, AND DISULFIDE BONDS.			
RC	TISSUE=Venom;			
RC	MEDLINE=93157385; PubMed=8430107;			
RA	Usami Y., Fujimura Y., Suzuki M., Ozeki Y., Nishio K., Fukui H.,			
RA	Titani K.;			
RA	"Primary structure of two-chain botrocetin, a von Willebrand factor			
RT	modulator purified from the venom of Bothrops jararaca.";			
RL	Proc. Natl. Acad. Sci. U.S.A. 90:928-932(1993).			
[2]				
RN	SEQUENCE OF 1-40.			
RC	TISSUE=Venom;			
RC	MEDLINE=91129280; PubMed=1993206;			
RA	Fujimura Y., Titani K., Usami Y., Suzuki M., Oyama R., Matsui T.,			
RA	Fukui H., Sugimoto M., Ruggeri Z.M.;			
RT	"Isolation and chemical characterization of two structurally and			
RT	functionally distinct forms of botrocetin, the platelet coagglutinin			
RT	isolated from the venom of Bothrops jararaca.";			
RL	Biochemistry 30:1957-1964(1991).			
[3]				
RN	X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS).			
RP	MEDLINE=22118144; PubMed=12121649;			
RA	Fukuda K., Doggett T.A., Bankston L.A., Cruz M.A., Diacovo T.G.,			
RA	Liddington R.C.;			
RT	"Structural basis of von Willebrand factor activation by the snake			
RT	toxin botrocetin.";			
RL	Structure 10:943-950(2002).			
CC	-!- FUNCTION: Two-chain Botrocetin forms an activated complex with			
CC	vWF, and the complex then binds to platelet GPIb, resulting in			
CC	platelet agglutination.			
CC	-!- FUNCTION: There are two distinct forms of the von Willebrand			
CC	factor-dependent platelet coagglutinin. The dimeric form is			
CC	34-times more active than the one-chain Botrocetin in promoting			
CC	vWF binding to platelets.			
CC	-!- SUBUNIT: Disulfide-linked dimer of an alpha and a beta chain.			
CC	vWF and Botrocetin form a soluble complex.			
CC	-!- SUBCELLULAR LOCATION: Secreted.			
CC	-!- SIMILARITY: Contains 1 C-type lectin family domain.			
DR	PIR; A47267; A47267.			
DR	PDB; 1JJK; 17-JUL-02.			
DR	PDB; 1FVU; 14-FEB-01.			
DR	InterPro; IPR002353; AntifreezeII.			
DR	InterPro; IPR001304; Lectin_C.			
DR	Pfam; PF00059; lectin_c_1.			
DR	PRINTS; PR00356; ANTIFREEZEII.			
DR	SMART; SM00034; CLECT; 1.			
DR	PROSITE; PS00615; C_TYPE_LECTIN_1; 1.			
DR	PROSITE; PS50041; C_TYPE_LECTIN_2; 1.			
KW	Lectin; 3D-structure.			

FT DISULFID 2 13
 FT DISULFID 30 128
 FT DISULFID 80 80
 FT DISULFID 103 120
 SQ SEQUENCE 133 AA; 15215 MW; B4CF4502946AC74B CRC64;
 INTERCHAIN (WITH C-75 IN BETA CHAIN).

Query Match 68.8%; Score 117; DB 1; Length 133;
 Best Local Similarity 65.5%; Pred. No. 1.2e-08;
 Matches 19; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

QY 1 DCSWSSYEGHCYKVFQSKTWTDAESF 29
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 Db 1 DCPGSSYEGNCYKFFQQRWADAERF 29

RESULT 8

ABBB TRIAB STANDARD; PRT; 118 AA.
 AC P81116;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Alboaggregin B beta subunit.
 OS Trimeresurus albolabris (White-lipped pit viper).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
 OC Viperidae; Crotalinae; Trimeresurus.
 OX NCBI_TaxID=8765;
 RN [1]
 RP SEQUENCE.

RC TISSUE=Venom;
 RX MEDLINE=98189535; PubMed=9531050;
 RA Kowalska M.A., Tan L., Holt J.C., Peng M., Karczewski J.,
 RA Calvete J.J., Niewiarowski S.;
 RT "Alboaggregins A and B. Structure and interaction with human
 platelets.";
 RL Thromb. Haemost. 79:609-613(1998).
 CC -!- FUNCTION: Binds to platelet GPIb/IX receptor system and stimulates
 agglutination.

CC -!- SUBUNIT: Heterodimer of alpha and beta subunits, disulfide-linked.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: Contains 1 C-type lectin family domain.
 DR HSP; P23807; IIXX.
 DR InterPro: IPR001304; Lectin_C.
 DR Pfam: PF00059; lectin_c; 1.
 DR SMART: SM00034; CLECT; 1.

DR PROSITE; PS00615; C-TYPE LECTIN 1; FALSE_NEG.
 DR PROSITE; PS50041; C-TYPE LECTIN_2; 1.
 KW Lectin.
 FT DOMAIN 1 118 C-TYPE LECTIN (LONG FORM).
 FT DISULFID 2 13 BY SIMILARITY.
 FT DISULFID 75 75 INTERCHAIN (WITH C-79 IN ALPHA CHAIN)
 FT (BY SIMILARITY).
 FT DISULFID 96 111 BY SIMILARITY.
 SQ SEQUENCE 118 AA; 13794 MW; 059EDFF6B474C4CE CRC64;

Query Match 68.2%; Score 116; DB 1; Length 118;
 Best Local Similarity 65.5%; Pred. No. 1.5e-08;
 Matches 19; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 1 DCSWSSYEGHCYKVFQSKTWTDAESF 29
 ||| |||||: |||||: |||||
 Db 1 DCPGSSYDLYCYKVFQQRWADAERF 29

RESULT 9

CVXB CRODU STANDARD; PRT; 148 AA.
 AC O93427;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Convulxin beta precursor (CVX beta).

OS Crotalus durissus terrificus (South American rattlesnake).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
 OC Viperidae; Crotalinae; Crotalus.
 OX NCBI_TaxID=8732;
 RN [1]
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 24-53; 99-109 AND 126-145.
 RC TISSUE=Venom gland;
 RX MEDLINE=98324901; PubMed=9657980;
 RA Leduc M., Bon C.;
 RT "Cloning of subunits of convulxin, a collagen-like platelet-
 aggregating protein from Crotalus durissus terrificus venom.";
 RL Biochem. J. 333:389-393(1998).
 CC -!- FUNCTION: Binds to the platelet and collagen receptor,
 glycoprotein VI (GPVI).
 CC -!- SUBUNIT: Heterohexamer of three alpha chains and three beta
 chains; disulfide-linked.
 CC -!- SIMILARITY: Contains 1 C-type lectin family domain.

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 between the Swiss Institute of Bioinformatics and the EMBL outstation
 at the European Bioinformatics Institute. There are no restrictions on its
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 entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 or send an email to license@isb-sib.ch).

EMBL; Y16349; CAA76182.1; --
 DR HSP; P23807; IIXX.
 DR InterPro: IPR001304; Lectin_C.
 DR Pfam: PF00059; lectin_c; 1.
 DR SMART; SM00034; CLECT; 1.
 DR PROSITE; PS00615; C-TYPE LECTIN 1; 1.
 DR PROSITE; PS50041; C-TYPE LECTIN_2; 1.
 KW Lectin; Glycoprotein; Signal.
 FT SIGNAL 1 23
 FT CHAIN 24 148 CONVULXIN BETA.
 FT DOMAIN 34 145 C-TYPE LECTIN.
 FT DISULFID 26 26 INTERCHAIN (WITH C-158 IN ALPHA CHAIN)
 FT (POTENTIAL).
 FT DISULFID 27 38 BY SIMILARITY.
 FT DISULFID 55 144 BY SIMILARITY.
 FT DISULFID 100 100 INTERCHAIN (WITH C-104 IN ALPHA CHAIN)
 FT (POTENTIAL).
 FT DISULFID 121 136 BY SIMILARITY.
 SQ SEQUENCE 148 AA; 17402 MW; 94D7E3E1BC693B9F CRC64;

Query Match 68.2%; Score 116; DB 1; Length 148;
 Best Local Similarity 67.9%; Pred. No. 1.8e-08;
 Matches 19; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

QY 2 CSDSSSYEGHCYKVFQSKTWTDAESF 29
 ||| |||||: |||||: |||||
 Db 27 CFSHSSYDRYCYKVFQQRWADAERF 54

RESULT 10

ECHB ECHCA STANDARD; PRT; 123 AA.
 AC P81996;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Echicetin beta subunit.

OS Echis carinatus (Saw-scaled viper).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
 OC Viperidae; Viperinae; Echis.
 OX NCBI_TaxID=40353;
 RN [1]
 RP SEQUENCE.

RC TISSUE=Venom;
 RX MEDLINE=95091801; PubMed=7999097;

Peng M., Holt J.C., Niewiarowski S.;
"Isolation, characterization and amino acid sequence of echicetin beta
subunit, a specific inhibitor of von Willebrand factor and thrombin
interaction with glycoprotein Ib.";
Biochem. Biophys. Res. Commun. 205:68-72(1994).
[2]
RN
RP
RQ
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YV
YW
YX
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ZL
ZM
ZN
ZO
ZP
ZQ
ZR
ZS
ZT
ZU
ZV
ZW
ZX
ZY
ZZ

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Best Local Similarity 58.6%; Pred. No. 5.5e-08;
Matches 17; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

QY 1 DCSDSWSSYEGHCYKVFQSKTWTDAESF 29
Db 1 DCPDSWSSFKQCYQIVKELKTWDEAEXF 29

RESULT 13
CHBA_CROHO
ID CHBA_CROHO STANDARD; PRT; 127 AA.
AC P81508;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE CHB-B alpha subunit.
OS Crotalus horridus horridus (timber rattlesnake).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Crotalinae; Crotalus.
OX NCBI_TaxID=8747;
RN [1]
RP SEQUENCE.
TISSUE=Venom;
RC MEDLINE=96420502; PubMed=8823201;
RA Andrews R.K., Kroll M.H., Ward C.M., Rose J.W., Scarborough R.M.,
RA Smith A.I., Lopez J.A., Berndt M.C.;
RT "Binding of a novel 50-kilodalton alphaaggregin from Trimeresurus
RT albolabris and related viper venom proteins to the platelet membrane
RT glycoprotein Ib-IX-V complex. Effect on platelet aggregation and
RT glycoprotein Ib-mediated platelet activation."
RL Biochemistry 35:12629-12639(1996).
CC 1- FUNCTION: Binds to platelet GPIB/IX receptor system, inhibits VWF
CC binding, and stimulates agglutination.
CC 1- SUBUNIT: Heterodimer of alpha and beta subunits; disulfide-linked.
CC 1- SUBCELLULAR LOCATION: Secreted.
CC 1- SIMILARITY: Contains 1 C-type lectin family domain.
DR PROSITE; PS00615; C_TYPE_LLECTIN_1; FALSE_NEG.
DR PROSITE; PS50041; C_TYPE_LLECTIN_2; 1.
KW Lectin.
FT DOMAIN 11 121 C-TYPE LECTIN.
FT DISULFID 4 15 BY SIMILARITY.
FT DISULFID 32 120 BY SIMILARITY.
FT DISULFID 81 81 INTERCHAIN (WITH C-92 IN BETA CHAIN)
FT (POTENTIAL).
FT DISULFID 95 112 BY SIMILARITY.
SQ SEQUENCE 127 AA; 15162 MW; B5DA100D383E3547 CRC64;

Query Match 65.3%; Score 111; DB 1; Length 127;
Best Local Similarity 62.1%; Pred. No. 7.1e-08;
Matches 18; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

QY 1 DCSDSWSSYEGHCYKVFQSKTWTDAESF 29
Db 3 ECPGWSYDRYCYKFKQEMTWDAERF 31

RESULT 14
ECHA_ECHA
ID ECHA_ECHA STANDARD; PRT; 133 AA.
AC P81017;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Echicetin alpha subunit.
OS Echis carinatus (Saw-scaled viper).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Viperinae; Echis.
OX NCBI_TaxID=40353;
RN [1]
RP SEQUENCE.
TISSUE=Venom;
RC MEDLINE=98104052; PubMed=9443815;
RA Yamada D., Morita T.;
RT "Purification and characterization of a Ca2+-dependent prothrombin
RT activator, multactivase, from the venom of Echis multisquamatus."
RL J. Biochem. 122:991-997(1997).
CC 1- FUNCTION: Multactivase, a carinactivase-like calcium dependent
CC prothrombin activator, activates prothrombin via recognition of
CC the calcium ion bound conformation of its gamma-carboxyglutamic
CC acid (GLA) domain.
CC 1- DOMAIN: Composed of a catalytic subunit with metalloprotease
CC activity and a regulatory subunit comprising two homologous

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TISSUE=Venom;
RC MEDLINE=97250657; PubMed=9163349;
RA Polgar J., Magnenat E.M., Peitsch M.C., Wells T.N.C., Sagi M.S.A.,
RA Clemetson K.J.;
RT "Amino acid sequence of the alpha subunit and computer modelling of
RT the alpha and beta subunits of echicetin from the venom of Echis
RL carinatus (saw-scaled viper).";
RL Biochem. J. 323:533-537(1997).
RN [2]
RP CHARACTERIZATION.
TISSUE=Venom;
RC MEDLINE=93244424; PubMed=8481512;
RA Peng M., Lu W., Bevilgia L., Niewiarowski S., Kirby E.P.;
RT "Echicetin: a snake venom protein that inhibits binding of von
RT Willebrand factor and alphaaggregins to platelet glycoprotein Ib."
RL Blood 81:2321-2328(1993).
CC 1- FUNCTION: Binds to platelet GPIb and inhibits platelet
CC agglutination.
CC 1- SUBUNIT: Heterodimer of alpha and beta subunits.
CC 1- SUBCELLULAR LOCATION: Secreted.
CC 1- SIMILARITY: Contains 1 C-type lectin family domain.
DR HSSP; P23806; 11XX.
DR InterPro; IPR001304; Lectin_C.
DR InterPro; IPR003990; Pancreatins_ac.
DR Pfam; PF00059; lectin_C; 1.
DR PRINTS; PR01504; PNCREATITSAP.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS00615; C_TYPE_LLECTIN_1; FALSE_NEG.
DR PROSITE; PS50041; C_TYPE_LLECTIN_2; 1.
KW Lectin.
FT DISULFID 4 15 BY SIMILARITY.
FT DISULFID 31 127 BY SIMILARITY.
FT DISULFID 102 119 BY SIMILARITY.
FT DISULFID 81 81 INTERCHAIN (WITH C-75 IN BETA CHAIN) (BY
FT SIMILARITY)
SQ SEQUENCE 133 AA; 15803 MW; 8F11C2D0BDC70B16 CRC64;

Query Match 60.3%; Score 102.5; DB 1; Length 133;
Best Local Similarity 58.6%; Pred. No. 9.6e-07;
Matches 17; Conservative 5; Mismatches 6; Indels 1; Gaps 1;

QY 1 DCSDSWSSYEGHCYKVFQSKTWTDAESF 29
Db 3 DCLSGWSFYEGHCYQLFR-LKTWDEAEKY 30

RESULT 15
MULR_ECHML
ID MULR_ECHML STANDARD; PRT; 29 AA.
AC P81798;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Multactivase regulatory subunit (fragment).
OS Echis multisquamatus (Central Asian sand viper).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Viperinae; Echis.
OX NCBI_TaxID=93050;
RN [1]
RP SEQUENCE.
TISSUE=Venom;
RC MEDLINE=98104052; PubMed=9443815;
RA Yamada D., Morita T.;
RT "Purification and characterization of a Ca2+-dependent prothrombin
RT activator, multactivase, from the venom of Echis multisquamatus."
RL J. Biochem. 122:991-997(1997).
CC 1- FUNCTION: Multactivase, a carinactivase-like calcium dependent
CC prothrombin activator, activates prothrombin via recognition of
CC the calcium ion bound conformation of its gamma-carboxyglutamic
CC acid (GLA) domain.
CC 1- DOMAIN: Composed of a catalytic subunit with metalloprotease
CC activity and a regulatory subunit comprising two homologous

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CC      polypeptides bound by S-S bridge(s).
DR      PIR; PC4421; PC4421.
KW      Prothrombin activator; Calcium.
FT      NON_TER      29
SQ      SEQUENCE      29 AA; 3458 MW; DFCA64AD1BC22882 CRC64;

Query Match      59.1%; Score 100.5; DB 1; Length 29;
Best Local Similarity 65.5%; Pred. No. 3.9e-07;
Matches 19; Conservative 0; Mismatches 9; Indels 1; Gaps 1;

QY      1 DCSSDWSYEGHCYKVFQSKTWTDAESF 29
      |||||
Db      1 DCLPGWSVTEGRCYKVFNQ-KIWKAAEKF 28

Search completed: December 8, 2003, 09:53:10
Job time : 5.14476 secs
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 8, 2003, 09:49:24 ; Search time 14.0857 Seconds
(without alignments)
531.285 Million cell updates/sec

Title: US-09-938-114-3
Perfect score: 170
Sequence: 1 DCSSDMSYEGHCYKVKQSKTWTDAESG 29

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_23:*

1: sp_archaea:*

2: sp_bacteria:*

3: sp_fungi:*

4: sp_human:*

5: sp_invertebrate:*

6: sp_mammal:*

7: sp_mhc:*

8: sp_organelle:*

9: sp_phage:*

10: sp_plant:*

11: sp_rodent:*

12: sp_virus:*

13: sp_vertebrate:*

14: sp_unclassified:*

15: sp_rvirus:*

16: sp_bacteriap:*

17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	163	95.9	152	13 Q9IAM1	Q9iam1 agkistrodon
2	155	91.2	152	13 Q9DEF9	Q9def9 agkistrodon
3	155	91.2	152	13 Q8JIW0	Q8jiw0 agkistrodon
4	148	87.1	146	13 Q8AYA4	Q8aya4 agkistrodon
5	136	80.0	146	13 Q9IAM0	Q9iam0 agkistrodon
6	134	78.8	146	13 Q9IY92	Q9iy92 agkistrodon
7	133	78.2	146	13 Q9DEF8	Q9def8 agkistrodon
8	133	78.2	146	13 Q8JIW7	Q8jiw7 agkistrodon
9	132	77.6	146	13 Q98SM5	Q98sm5 agkistrodon
10	132	77.6	146	13 Q8JIW1	Q8jiw1 agkistrodon
11	127	74.7	146	13 Q9DG31	Q9dg31 agkistrodon
12	124	72.9	146	13 Q9I840	Q9i840 agkistrodon
13	124	72.9	155	13 Q8JIW8	Q8jiw8 agkistrodon
14	123	72.4	131	13 Q98SM9	Q98sm9 echis carin
15	123	72.4	146	13 Q98U00	Q98u00 trimeresuru
16	121	71.2	124	13 Q90WL9	Q90wl9 agkistrodon

17	120	70.6	33	13 Q9PRQ7	Q9prq7 bothrops ja
18	120	70.6	123	13 Q9PSM5	Q9psm5 bothrops ja
19	119	70.0	145	13 Q9YGN4	Q9ygn4 agkistrodon
20	119	70.0	152	13 Q9DG39	Q9dg39 agkistrodon
21	118	69.4	125	13 Q9PSM8	Q9psm8 echis carin
22	116	68.2	30	13 Q9PRP7	Q9prp7 echis carin
23	116	68.2	146	13 Q9DEA1	Q9dea1 agkistrodon
24	116	68.2	40	13 Q9PS19	Q9ps19 trimeresuru
25	115	67.6	149	13 Q8UVC7	Q8uvc7 agkistrodon
26	114	67.1	149	13 Q8AYA3	Q8aya3 agkistrodon
27	112	65.9	30	13 Q9PS06	Q9ps06 bothrops ja
28	104	61.2	40	13 Q9PS20	Q9ps20 trimeresuru
29	103	60.6	136	13 Q9I841	Q9i841 agkistrodon
30	103	60.6	154	13 Q8JIV9	Q8jiv9 agkistrodon
31	102	60.0	146	13 Q8JG76	Q8jgt6 trimeresuru
32	102	60.0	148	13 Q8AV38	Q8av38 trimeresuru
33	100	58.8	158	13 Q8JG77	Q8jgt7 trimeresuru
34	99	58.2	157	13 Q9YGN5	Q9ygn5 agkistrodon
35	99	58.2	157	13 Q9YGN5	Q9ygn5 agkistrodon
36	99	58.2	157	13 Q9YGN5	Q9ygn5 agkistrodon
37	99	58.2	157	13 Q9YGN5	Q9ygn5 agkistrodon
38	97	57.1	30	13 Q9PS05	Q9ps05 bothrops ja
39	95	55.9	2109	13 P79787	P79787 gallus gall
40	94	55.3	158	13 Q8UVC6	Q8uvc6 agkistrodon
41	94	55.3	158	13 Q8AYA5	Q8aya5 agkistrodon
42	93	54.7	155	13 Q9DEA2	Q9dea2 agkistrodon
43	92	54.1	719	6 O62623	O62623 bos taurus
44	91	53.5	135	13 Q9PSM4	Q9psm4 lachesis mu
45	90	52.9	42	13 Q9PRQ8	Q9prq8 bothrops ja

ALIGNMENTS

RESULT 1

Q9IAM1 ID Q9IAM1 PRELIMINARY; PRT; 152 AA.

AC Q9IAM1;

DT 01-OCT-2000 (TrEMBLrel. 15, Created)

DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)

DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)

DE Agkisacutacin A chain.

OS Agkistrodon acutus (Hundred-pace snake) (Deinagkistrodon acutus).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;

OC Viperidae; Crotalinae; Deinagkistrodon.

OX NCBI_TaxID=36307;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Venom;

RA Yu H.-X., Xiang K.-J., Liu J.;

RT "cDNA sequencing and analysis of eleven C-type lectin-like protein subunits from Agkistrodon acutus."

RL Chin. J. Biochem. Biophys. 0:0-0(2002).

DR EMBL; AF176420; AAF26286.2; -

DR HSSP; P23806; 11XX.

DR InterPro; IPR001304; Lectin C.

DR Pfam; PF00059; lectin_c; 1.

DR SMART; SM00034; CLECT_1

DR PROSITE; PS00615; C-TYPE LECTIN 1; 1.

DR PROSITE; PS00041; C-TYPE LECTIN 2; 1.

SQ SEQUENCE 152 AA; 17109 MW; 76A0F636DBF0D7AB CRC64;

Query Match 95.9%; Score 163; DB 13; Length 152;
Best Local Similarity 96.6%; Pred. No. 1.5e-15;
Matches 28; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DCSSDMSYEGHCYKVKQSKTWTDAESF 29

Db 24 DCSSGSSSYEGHCYKVKQSKTWTDAESF 52

RESULT 2

[illegible]

DR PROSITE; PS00615; C TYPE LECTIN 1; 1.
 DR PROSITE; PS50041; C_TYPE LECTIN_2; 1.
 SQ SEQUENCE 146 AA; 736086D6864131BB CRC64;
 Query Match 80.0%; Score 136; DB 13; Length 146;
 Best Local Similarity 75.9%; Pred. No. 1e-11;
 Matches 22; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DCSSDSSSYEGHCYKVFQSKTWTDAESF 29
 ||| ||||| ||||| ||||| : ||| |||
 Db 24 DCPDSSSYEGHCYKVFQSKTWTDAESF 52
 ||| ||||| ||||| ||||| : ||| |||
 RESULT 6
 Q9YI92 SEQUENCE FROM N.A. PRT; 146 AA.
 ID Q9YI92 PRELIMINARY;
 AC Q9YI92;
 DT 01-MAY-1999 (TrEMBLrel. 10, Created)
 DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
 DE Mamushigin beta
 OS Agkistrodon halys blomhoffi (Mamushi) (Gloydius blomhoffii).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
 OC Viperidae; Crotalinae; Agkistrodon.
 OX NCBI_TaxID=61300;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98319530; PubMed=9657448;
 RA Sakurai Y., Fujimura Y., Kokubo T., Imamura K., Kawasaki T., Handa M.,
 RA Suzuki M., Matsui T., Titani K., Yoshioaka A.;
 RT "The cDNA cloning and molecular characterization of a snake venom
 RT platelet glycoprotein Ib-binding protein, mamushigin, from Agkistrodon
 RT halys blomhoffii venom.";
 RL Thromb. Haemost. 79:1199-1207(1998).
 DR EMBL; AB019616; BAA34425.1; -.
 DR HSSP; P23807; 11XX.
 DR InterPro; IPR001304; LECTIN_C.
 DR Pfam; PF00059; lectin_c; 1.
 DR SMART; SM00034; CLECT; 1.
 DR PROSITE; PS00615; C_TYPE LECTIN 1; 1.
 DR PROSITE; PS50041; C_TYPE LECTIN_2; 1.
 SQ SEQUENCE 146 AA; 17064 MW; 9EDA84BDC24E76D CRC64;
 Query Match 78.8%; Score 134; DB 13; Length 146;
 Best Local Similarity 72.4%; Pred. No. 1e-11;
 Matches 21; Conservative 3; Mismatches 5; Indels 0; Gaps 0;
 QY 1 DCSSDSSSYEGHCYKVFQSKTWTDAESF 29
 ||| ||||| ||||| ||||| : ||| |||
 Db 24 DCPDSSSYEGHCYKVFQSKTWTDAESF 52
 ||| ||||| ||||| ||||| : ||| |||
 RESULT 7
 Q9DF8 SEQUENCE FROM N.A. PRT; 146 AA.
 ID Q9DF8 PRELIMINARY;
 AC Q9DF8;
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Anticoagulant protein-B precursor.
 GN ACP-B.
 OS Agkistrodon acutus (Hundred-pace snake) (Deinagkistrodon acutus).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
 OC Viperidae; Crotalinae; Deinagkistrodon.
 OX NCBI_TaxID=36307;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Venom gland;
 RA Tani A., Nose T., Nikandrov N.N., Ogawa T., Deshimaru M., Fukumaki Y.,
 RA Chang C., Shimohigashi Y., Ohno M.;
 RT "Purification, sequencing, and cDNA cloning of a heterodimeric

RT antioagulant protein from Deinagkistrodon acutus venom gland.";
 RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB036881; BAB20441.1; -.
 DR HSSP; P23807; 11XX.
 DR InterPro; IPR001304; LECTIN_C.
 DR InterPro; IPR003990; Pancreatins_ac.
 DR Pfam; PF00059; lectin_c; 1.
 DR PRINTS; PR01504; PNCREATITSAP.
 DR SMART; SM00034; CLECT; 1.
 DR PROSITE; PS00615; C_TYPE LECTIN 1; 1.
 DR PROSITE; PS50041; C_TYPE LECTIN_2; 1.
 KW Signal.
 FT SIGNAL 1 23 POTENTIAL.
 SQ SEQUENCE 146 AA; 16997 MW; 420D71EBE4E9F5D2 CRC64;
 Query Match 78.2%; Score 133; DB 13; Length 146;
 Best Local Similarity 72.4%; Pred. No. 2.7e-11;
 Matches 21; Conservative 2; Mismatches 6; Indels 0; Gaps 0;
 QY 1 DCSSDSSSYEGHCYKVFQSKTWTDAESF 29
 ||| ||||| ||||| ||||| : ||| |||
 Db 24 DCPDSSSYEGHCYKVFQSKTWTDAESF 52
 ||| ||||| ||||| ||||| : ||| |||
 RESULT 8
 Q8JIV7 PRELIMINARY; PRT; 146 AA.
 ID Q8JIV7 PRELIMINARY;
 AC Q8JIV7;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE ACF 1/2 B-chain.
 OS Agkistrodon acutus (Hundred-pace snake) (Deinagkistrodon acutus).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
 OC Viperidae; Crotalinae; Deinagkistrodon.
 OX NCBI_TaxID=36307;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Yu H., Xiang K., Wang Y., Liu J.;
 RT "B chain of ACF 1/2 from Deinagkistrodon acutus.";
 RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY091761; AAM22789.1; -.
 DR InterPro; IPR001304; LECTIN_C.
 DR InterPro; IPR003990; Pancreatins_ac.
 DR Pfam; PF00059; lectin_c; 1.
 DR PRINTS; PR01504; PNCREATITSAP.
 DR SMART; SM00034; CLECT; 1.
 DR PROSITE; PS00615; C_TYPE LECTIN 1; 1.
 DR PROSITE; PS50041; C_TYPE LECTIN_2; 1.
 SQ SEQUENCE 146 AA; 16925 MW; F2493CACBA5D2144 CRC64;
 Query Match 78.2%; Score 133; DB 13; Length 146;
 Best Local Similarity 72.4%; Pred. No. 2.7e-11;
 Matches 21; Conservative 2; Mismatches 6; Indels 0; Gaps 0;
 QY 1 DCSSDSSSYEGHCYKVFQSKTWTDAESF 29
 ||| ||||| ||||| ||||| : ||| |||
 Db 24 DCPDSSSYEGHCYKVFQSKTWTDAESF 52
 ||| ||||| ||||| ||||| : ||| |||
 RESULT 9
 Q98SM5 PRELIMINARY; PRT; 124 AA.
 ID Q98SM5 PRELIMINARY;
 AC Q98SM5;
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE Agkisin-b.
 OS Agkistrodon acutus (Hundred-pace snake) (Deinagkistrodon acutus).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
 OC Viperidae; Crotalinae; Deinagkistrodon.

```

OX NCBI_TaxID=36307;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Venom gland;
RA Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
RL EMBL; AF350324; AAK26430.1; -.
DR HSSP; P23807; IIXX.
DR InterPro; IPR001304; Lectin_C.
DR Pfam; PF00059; lectin_c; 1.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS00615; C_TYPE_LLECTIN_1; 1.
DR PROSITE; PS50041; C_TYPE_LLECTIN_2; 1.
SQ SEQUENCE 124 AA; 14701 MW; 46B2D580CB3DC518 CRC64;

Query Match 77.6%; Score 132; DB 13; Length 124;
Best Local Similarity 72.4%; Pred. No. 3.1e-11;
Matches 21; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 DCSSDSSSYEGHCYKVKQSKTWTDAESF 29
Db 2 DCPSESSSYEGHCYKPFNEKNWADAENF 30

RESULT 10
Q8J1W1
ID Q8J1W1 PRELIMINARY; PRT; 146 AA.
AC Q8J1W1
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Agkisutacin B-chain.
OS Agkisutrodon acutus (Hundred-pace snake) (Deinagkistrodon acutus).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Crotalinae; Deinagkistrodon.
OX NCBI_TaxID=36307;
RN [1]
RP SEQUENCE FROM N.A.
RA Yu H., Xiang X., Wang Y., Liu J.;
RT "B chain of agkisutacin from Deinagkistrodon acutus."
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY091756; AAM22785.1; -.
DR InterPro; IPR001304; Lectin_C.
DR Pfam; PF00059; Pancreatins_ac.
DR PRINTS; PR01504; PNCREATITSAP.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS00615; C_TYPE_LLECTIN_1; 1.
DR PROSITE; PS50041; C_TYPE_LLECTIN_2; 1.
SQ SEQUENCE 146 AA; 16740 MW; 6260B6D68741317C CRC64;

Query Match 77.6%; Score 132; DB 13; Length 146;
Best Local Similarity 72.4%; Pred. No. 3.7e-11;
Matches 21; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 DCSSDSSSYEGHCYKVKQSKTWTDAESF 29
Db 24 DCPSESSSYEGHCYKPFNEKNWADAENF 52

RESULT 11
Q9DG31
ID Q9DG31 PRELIMINARY; PRT; 146 AA.
AC Q9DG31
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Halysin B-chain precursor.
OS Agkisutrodon halys pallas (Chinese water moccasin) (Gloydius halys pallas).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;

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OC Viperidae; Crotalinae; Gloydius.
OX NCBI_TaxID=8714;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Venom;
RA Koo B.H., Sohn Y.D., Kim D.S., Jang Y.S., Chung K.H.;
RT "A Novel Coagulation Factor Xa Inhibitor from Korean Snake (Agkisutrodon halys) venom."
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF197915; AAG28522.1; -.
DR HSSP; P23807; IIXX.
DR InterPro; IPR001304; Lectin_C.
DR InterPro; IPR003990; Pancreatins_ac.
DR Pfam; PF00059; lectin_c; 1.
DR PRINTS; PR01504; PNCREATITSAP.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS00615; C_TYPE_LLECTIN_1; 1.
DR PROSITE; PS50041; C_TYPE_LLECTIN_2; 1.
KW SIGNAL.
FT CHAIN 1 23 POTENTIAL.
FT CHAIN 24 146 HALYXIN B-CHAIN.
SQ SEQUENCE 146 AA; 16841 MW; C47D8A43B0A00709 CRC64;

Query Match 74.7%; Score 127; DB 13; Length 146;
Best Local Similarity 69.0%; Pred. No. 1.9e-10;
Matches 20; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

QY 1 DCSSDSSSYEGHCYKVKQSKTWTDAESF 29
Db 24 DCPSESSSYEGHCYKPFNEKNWADAENF 52

RESULT 12
Q9I840
ID Q9I840 PRELIMINARY; PRT; 146 AA.
AC Q9I840
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Aggretin beta chain (fragment).
OS Agkisutrodon rhodostoma (Malayan pit viper) (Calloselasma rhodostoma).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Crotalinae; Calloselasma.
OX NCBI_TaxID=8717;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Venom gland;
RX MEDLINE=99443731; PubMed=10512747;
RA Chung C.H., Au L.C., Huang T.F.;
RT "Molecular cloning and sequence analysis of aggretin, a collagen-like platelet aggregation inducer."
RL Biochem. Biophys. Res. Commun. 263:723-727 (1999).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Venom gland;
RA Chung C.H., Au L.C., Huang T.F.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF244901; AAF79953.1; -.
DR HSSP; P23807; IIXX.
DR InterPro; IPR001304; Lectin_C.
DR Pfam; PF00059; Pancreatins_ac.
DR PRINTS; PR01504; PNCREATITSAP.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS00615; C_TYPE_LLECTIN_1; 1.
DR PROSITE; PS50041; C_TYPE_LLECTIN_2; 1.
FT NON TER 146
SQ SEQUENCE 146 AA; 16770 MW; 930839140CFD8908 CRC64;

Query Match 72.9%; Score 124; DB 13; Length 146;
Best Local Similarity 69.0%; Pred. No. 5.2e-10;
Matches 20; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

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QY 1 DCSSDSSYEGHCYKVFQSKTWTDAESF 29
 |||||:|||||:|||||
 Db 24 DCPGWSYEGHCYKVFQSKTWTDAESF 52
 |||||:|||||:|||||

RESULT 13
 Q8JIV8 PRELIMINARY; PRT; 155 AA.
 AC Q8JIV8;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE C-type lectin.
 OS Agkistrodon acutus (Hundred-pace snake) (Deinagkistrodon acutus).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
 OC Viperidae; Crotalinae; Deinagkistrodon.
 OX NCBI_TaxID=36307;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Yu H., Xiang K., Wang Y., Liu J.;
 RT "Member of C-type lectin family from Deinagkistrodon acutus.";
 RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY091760; AAM22788.1;
 DR InterPro; IPR001304; Lectin C.
 DR Pfam; PF00059; lectin_c; 1.
 DR PRINTS; PR01504; PNCREATITSAP.
 DR SMART; SM00034; CLECT; 1.
 DR PROSITE; PS00615; C_TYPE_LLECTIN_1; 1.
 DR PROSITE; PS50041; C_TYPE_LLECTIN_2; 1.
 KW Lectin.
 SQ SEQUENCE 155 AA; 17944 MW; 3E935FF53773AB94 CRC64;

Query Match
 Best Local Similarity 72.9%; Score 124; DB 13; Length 155;
 Matches 20; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

QY 1 DCSSDSSYEGHCYKVFQSKTWTDAESF 29
 |||||:|||||:|||||
 Db 24 DCPGWSYEGHCYKVFQSKTWTDAESF 52
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RESULT 14
 Q9PSM9 PRELIMINARY; PRT; 131 AA.
 AC Q9PSM9;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE ECLV IX/X-BP alpha SUBUNIT=COAGULATION factor IX/factor X-binding
 DE protein alpha subunit.
 OS Echis carinatus (Saw-scaled viper).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
 OC Viperidae; Viperinae; Echis.
 OX NCBI_TaxID=40353;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=96196635; PubMed=8611513;
 RA Chen Y.L., Tsai I.H.;
 RT "Functional and sequence characterization of coagulation factor
 RT IX/factor X-binding protein from the venom of Echis carinatus
 RT leucogaster.";
 RL Biochemistry 35:5264-5271(1996).
 DR HSP; P23806; IIXX.
 DR InterPro; IPR001304; Lectin C.
 DR Pfam; PF00059; lectin_c; 1.
 DR SMART; SM00034; CLECT; 1.
 DR PROSITE; PS00615; C_TYPE_LLECTIN_1; 1.
 DR PROSITE; PS50041; C_TYPE_LLECTIN_2; 1.
 SQ SEQUENCE 131 AA; 15439 MW; B85E6C5CBF317E24 CRC64;

Query Match
 Best Local Similarity 72.4%; Score 123; DB 13; Length 131;
 Matches 20; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

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 |||||:|||||:|||||
 Db 1 DCLPGWSYEGHCYKVFQSKTWTDAESF 29
 |||||:|||||:|||||

RESULT 15
 Q98UJ0 PRELIMINARY; PRT; 146 AA.
 ID Q98UJ0;
 AC Q98UJ0;
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
 DE Factor XI/factor X binding protein A chain.
 GN XI/XBP-A.
 OS Trimeresurus flavoviridis (Habu).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
 OC Viperidae; Crotalinae; Trimeresurus.
 OX NCBI_TaxID=88087;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Venom gland;
 RA Tani A., Ogawa T., Nose T., Nikandorov N.N., Deshimaru M., Chijiwa T.,
 RA Chang C., Fukumaki Y., Ohno M.;
 RT "Characterization and molecular evolution of an anticoagulant protein
 RT from Agkistrodon actus venom.";
 RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB046491; BAB21452.1;
 DR HSP; P23806; IIXX.
 DR InterPro; IPR001304; Lectin C.
 DR InterPro; IPR003990; Pncratiss_ac.
 DR Pfam; PF00059; lectin_c; 1.
 DR PRINTS; PR01504; PNCREATITSAP.
 DR SMART; SM00034; CLECT; 1.
 DR PROSITE; PS00615; C_TYPE_LLECTIN_1; 1.
 DR PROSITE; PS50041; C_TYPE_LLECTIN_2; 1.
 SQ SEQUENCE 146 AA; 16461 MW; 6ADF0E032544316C CRC64;

Query Match
 Best Local Similarity 74.1%; Score 123; DB 13; Length 146;
 Matches 20; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 DCSSDSSYEGHCYKVFQSKTWTDAE 27
 |||||:|||||:|||||
 Db 18 DCLSGWSYEGHCYKVFQSKTWTDAE 44
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Search completed: December 8, 2003, 09:54:48
 Job time : 14.0857 secs

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GenCore version 5.1.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: December 8, 2003, 13:34:19 : Search time 751.514 Seconds
(without alignments)
937.879 Million cell updates/sec

Title: US-09-938-114-3

Perfect score: 170

Sequence: 1 DCSDSWSSYEGHCYKVFQKSTWTDARSF 29

Scoring table: BLOSUM62

Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-DOCALLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEADSIZE=500 -MINLEN=0 -MAXLEN=2000000000
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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

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7: em_estro.*
8: em_htc.*
9: gb_estl.*
10: gb_est2.*
11: gb_htc.*
12: gb_est3.*
13: gb_est4.*
14: gb_est5.*
15: em_estfun.*
16: em_estom.*
17: em_gss_hum.*
18: em_gss_inv.*
19: em_gss_pln.*
20: em_gss_vrt.*
21: em_gss_fun.*
22: em_gss_mam.*
23: em_gss_mus.*
24: em_gss_pro.*
25: em_gss_rod.*
26: em_gss_pbg.*
27: em_gss_vrl.*
28: gb_gasl.*

29: gb_gss2.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
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3	127	74.7	391	12	BM401469	BM401469 JHLE03F S
4	127	74.7	475	12	BM401621	BM401621 JLIC02F S
5	127	74.7	504	12	BM401628	BM401628 JHLE12F S
6	127	74.7	510	12	BM401667	BM401667 JHLE12F S
7	127	74.7	512	12	BM401495	BM401495 JH2H07F S
8	121	71.2	343	12	BM401656	BM401656 JH2B09F S
9	120	70.6	633	12	BM401686	BM401686 JH2E04F S
10	119	70.0	378	12	BM401620	BM401620 PHO15FB S
11	119	70.0	574	12	BM401417	BM401417 GH061F S
12	119	70.0	654	12	BM401401	BM401401 GH025F S
13	117	68.8	301	12	BM401654	BM401654 JH2D07F S
14	115	67.6	460	12	BM401460	BM401460 JH1D06F S
15	112	65.9	374	12	BM401520	BM401520 JH2G02F S
16	112	65.9	497	12	BM401552	BM401552 JH3E12F S
17	100	58.8	406	12	BM401598	BM401598 JH4F11F S
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23	95	55.9	765	13	BU400634	BU400634 604137678
24	95	55.9	796	13	BU250042	BU250042 603403475
25	95	55.9	846	13	BU410105	BU410105 603158654
26	95	55.9	951	13	BU409519	BU409519 603159673
27	95	55.9	967	13	BU314865	BU314865 603487735
28	95	55.9	1022	13	BU127176	BU127176 603115043
29	94	55.3	389	12	BG897747	BG897747 HOA25-1-A
30	94	55.3	389	12	BG897804	BG897804 HOA25-1-H
31	94	55.3	426	12	BG901081	BG901081 HOA53-1-E
32	94	55.3	458	10	BE550485	BE550485 7a27b11.X
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34	94	55.3	644	12	BG899769	BG899769 HOA39-1-H
35	94	55.3	681	29	AG094039	AG094039 Pan crogl
36	94	55.3	706	12	BG329062	BG329062 HNC11-1-A
37	94	55.3	708	9	AI907207	AI907207 RC-BT133-
38	94	55.3	708	12	BG925582	BG925582 HNC30-1-C
39	94	55.3	723	12	BG929205	BG929205 HNC59-1-E
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41	91	53.5	598	13	BU323232	BU323232 603490804
42	91	53.5	702	13	BU266055	BU266055 603815327
43	91	53.5	703	13	BU269611	BU269611 603816223
44	91	53.5	726	13	BU230613	BU230613 603399651
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ALIGNMENTS

RESULT 1
BM401696
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

BM401696 172 bp mRNA linear EST 01-MAY-2002
PHIA01F Snake Bothrops insularis library IL2 Bothrops insularis
cDNA 5', similar to Snake venom C-type lectin, mRNA sequence.

BM401696
EST.
Bothrops insularis (island jataraca)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Lepidosauria; Squamata; Scieroglossa; Serpentes; Colubroidea;
Viperidae; Crotalinae; Bothrops.

REFERENCE
 AUTHORS
 TITLE

1 (bases 1 to 172)
 Junqueira-de-Azevedo, I.L.M. and Ho, P.L.
 A survey of gene expression and diversity in the venom glands of
 the pitviper snake Bothrops insularis through the generation of
 expressed sequence tags (ESTs)

JOURNAL
 MEDLINE
 PUBMED
 COMMENT

Gene 299 (1-2), 279-291 (2002)
 22347338
 12459276
 Contact: Paulo Lee Ho
 Instituto Butantan
 Av. Vital Brazil, 1500, Sao Paulo SP, BRAZIL, 05503-900
 Tel: 55 11 37 26 7222 ext. 2083
 Fax: 55 11 37 26 1505
 Email: hoplee@usp.br
 This EST corresponds to cluster BITL01A (see Reference)
 Seq primer: M13F.

FEATURES
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 Location/Qualifiers
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 /organism="Bothrops insularis"
 /mol_type="mRNA"
 /db_xref="taxon:8723"
 /tissue_type="venom glands"
 /clone_lib="Snake Bothrops insularis library IL2"
 /note="Organ: venom glands; Vector: pGEM11zf+; Site 1: Eco
 RI; Site 2: Not I; Sug of mRNA from Bothrops insularis
 venom glands were primed with oligo-(dT) and reverse
 transcribed to cDNA using Superscript Plasmid System for
 cDNA Synthesis and Cloning (Life Technologies). The cDNAs
 were selected by size (350-600 pb and up 600 pb) in
 agarose gel electrophoresis, linked to Eco RI adapters and
 directionally cloned in pGEM11zf+ vector (Promega). ESTs
 were generated from random clones and grouped in unique
 sequences. The putative identification of each EST or
 cluster was obtained through Blast searches (e-value <
 e-05)."

BASE COUNT 34 a 39 c 47 g 42 t 10 others
 ORIGIN

Alignment Scores:
 Pred. No.: 1.35e-09 Length: 172
 Score: 133.00 Matches: 21
 Percent Similarity: 79.31% Conservative: 2
 Best Local Similarity: 72.41% Mismatches: 6
 Query Match: 78.24% Indels: 0
 DB: 12 Gaps: 0

US-09-938-114-3 (1-29) x BM401696 (1-172)

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 Db 82 GATTGTCCCTCTGATTGTGTCCTATGAGGGCATTGCTACAGCTCTTCAACACGG 141
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Qy 21 LysThrTrpThrAspAlaGluSerPhe 29
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 Db 142 ATGAACTGGCGGATGCAGAGATT 168
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RESULT 2
 BM401618
 LOCUS
 DEFINITION
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM

BM401618 378 bp mRNA linear EST 01-MAY-2002
 JLI007F Snake Bothrops insularis library IL3 Bothrops insularis
 cDNA 5', similar to Snake venom C-type lectin, mRNA sequence.
 BM401618
 BM401618.1 GI:20376246
 EST.
 Bothrops insularis (island jararaca)
 Bothrops insularis
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
 Viperidae; Crotalinae; Bothrops.

REFERENCE
 AUTHORS
 TITLE

1 (bases 1 to 378)
 Junqueira-de-Azevedo, I.L.M. and Ho, P.L.
 A survey of gene expression and diversity in the venom glands of
 the pitviper snake Bothrops insularis through the generation of
 expressed sequence tags (ESTs)

JOURNAL
 MEDLINE
 PUBMED
 COMMENT

Gene 299 (1-2), 279-291 (2002)
 22347338
 12459276
 Contact: Paulo Lee Ho
 Instituto Butantan
 Av. Vital Brazil, 1500, Sao Paulo SP, BRAZIL, 05503-900
 Tel: 55 11 37 26 7222 ext. 2083
 Fax: 55 11 37 26 1505
 Email: hoplee@usp.br
 This EST corresponds to cluster BITL01A (see Reference)
 Seq primer: M13F.

FEATURES
 source
 Location/Qualifiers
 1..378
 /organism="Bothrops insularis"
 /mol_type="mRNA"
 /db_xref="taxon:8723"
 /tissue_type="venom glands"
 /clone_lib="Snake Bothrops insularis library IL3"
 /note="Organ: venom glands; Vector: pGEM11zf+; Site 1: Eco
 RI; Site 2: Not I; Sug of mRNA from Bothrops insularis
 venom glands were primed with oligo-(dT) and reverse
 transcribed to cDNA using Superscript Plasmid System for
 cDNA Synthesis and Cloning (Life Technologies). The cDNAs
 were selected by size (350-600 pb and up 600 pb) in
 agarose gel electrophoresis, linked to Eco RI adapters and
 directionally cloned in pGEM11zf+ vector (Promega). ESTs
 were generated from random clones and grouped in unique
 sequences. The putative identification of each EST or
 cluster was obtained through Blast searches (e-value <
 e-05)."

BASE COUNT 88 a 91 c 102 g 95 t 2 others
 ORIGIN

Alignment Scores:
 Pred. No.: 3.12e-08 Length: 378
 Score: 127.00 Matches: 20
 Percent Similarity: 78.57% Conservative: 2
 Best Local Similarity: 71.43% Mismatches: 6
 Query Match: 74.71% Indels: 0
 DB: 12 Gaps: 0

US-09-938-114-3 (1-29) x BM401618 (1-378)

Qy 1 AspCysSerSerAspTrpSerTyrGluGlyHisCysTyrLysValPheLysGlnSer 20
 |||||
 Db 78 GATTGTCCCTCTGATTGTGTCCTATGAGGGCATTGCTACAGCTCTTCAACACGG 137
 |||||

Qy 21 LysThrTrpThrAspAlaGluSer 28
 |||||
 Db 138 ATGAACTGGCGGATGCAGAGATT 161
 |||||

RESULT 3
 BM401469
 LOCUS
 DEFINITION
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM

BM401469 391 bp mRNA linear EST 01-MAY-2002
 JHIE09F Snake Bothrops insularis library IL3 Bothrops insularis
 cDNA 5', similar to Snake venom C-type lectin, mRNA sequence.
 BM401469
 BM401469.1 GI:20376097
 EST.
 Bothrops insularis (island jararaca)
 Bothrops insularis
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
 Viperidae; Crotalinae; Bothrops.

REFERENCE
 AUTHORS
 TITLE

1 (bases 1 to 391)
 Junqueira-de-Azevedo, I.L.M. and Ho, P.L.
 A survey of gene expression and diversity in the venom glands of
 the pitviper snake Bothrops insularis through the generation of
 expressed sequence tags (ESTs)

JOURNAL
 MEDLINE
 PUBMED
 COMMENT

Gene 299 (1-2), 279-291 (2002)

the pitviper snake Bothrops insularis through the generation of
 expressed sequence tags (ESTs)

JOURNAL
 MEDLINE
 PUBMED
 COMMENT

Gene 299 (1-2), 279-291 (2002)
 22347338
 12459276
 Contact: Paulo Lee Ho
 Instituto Butantan
 Av. Vital Brazil, 1500, Sao Paulo SP, BRAZIL, 05503-900
 Tel: 55 11 37 26 7222 ext. 2083
 Fax: 55 11 37 26 1505
 Email: hoplee@usp.br
 This EST corresponds to cluster BITL01A (see Reference)
 Seq primer: M13F.

FEATURES
 source
 Location/Qualifiers
 1..378
 /organism="Bothrops insularis"
 /mol_type="mRNA"
 /db_xref="taxon:8723"
 /tissue_type="venom glands"
 /clone_lib="Snake Bothrops insularis library IL3"
 /note="Organ: venom glands; Vector: pGEM11zf+; Site 1: Eco
 RI; Site 2: Not I; Sug of mRNA from Bothrops insularis
 venom glands were primed with oligo-(dT) and reverse
 transcribed to cDNA using Superscript Plasmid System for
 cDNA Synthesis and Cloning (Life Technologies). The cDNAs
 were selected by size (350-600 pb and up 600 pb) in
 agarose gel electrophoresis, linked to Eco RI adapters and
 directionally cloned in pGEM11zf+ vector (Promega). ESTs
 were generated from random clones and grouped in unique
 sequences. The putative identification of each EST or
 cluster was obtained through Blast searches (e-value <
 e-05)."

BASE COUNT 88 a 91 c 102 g 95 t 2 others
 ORIGIN

Alignment Scores:
 Pred. No.: 3.12e-08 Length: 378
 Score: 127.00 Matches: 20
 Percent Similarity: 78.57% Conservative: 2
 Best Local Similarity: 71.43% Mismatches: 6
 Query Match: 74.71% Indels: 0
 DB: 12 Gaps: 0

US-09-938-114-3 (1-29) x BM401618 (1-378)

Qy 1 AspCysSerSerAspTrpSerTyrGluGlyHisCysTyrLysValPheLysGlnSer 20
 |||||
 Db 78 GATTGTCCCTCTGATTGTGTCCTATGAGGGCATTGCTACAGCTCTTCAACACGG 137
 |||||

Qy 21 LysThrTrpThrAspAlaGluSer 28
 |||||
 Db 138 ATGAACTGGCGGATGCAGAGATT 161
 |||||

RESULT 3
 BM401469
 LOCUS
 DEFINITION
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM

BM401469 391 bp mRNA linear EST 01-MAY-2002
 JHIE09F Snake Bothrops insularis library IL3 Bothrops insularis
 cDNA 5', similar to Snake venom C-type lectin, mRNA sequence.
 BM401469
 BM401469.1 GI:20376097
 EST.
 Bothrops insularis (island jararaca)
 Bothrops insularis
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
 Viperidae; Crotalinae; Bothrops.

REFERENCE
 AUTHORS
 TITLE

1 (bases 1 to 391)
 Junqueira-de-Azevedo, I.L.M. and Ho, P.L.
 A survey of gene expression and diversity in the venom glands of
 the pitviper snake Bothrops insularis through the generation of
 expressed sequence tags (ESTs)

JOURNAL
 MEDLINE
 PUBMED
 COMMENT

Gene 299 (1-2), 279-291 (2002)

MEDLINE
12459276
PUBMED
COMMENT

Contact: Paulo Lee Ho
Centro de Biotecnologia
Instituto Butantan

Av. Vital Brazil, 1500, Sao Paulo SP, BRAZIL, 05503-900
Tel: 55 11 37 26 7222 ext. 2083
Fax: 55 11 37 26 1505
Email: hoplee@usp.br

This EST corresponds to cluster BITL03A (see Reference)
Seq primer: M13F.

Location/Qualifiers
1. .391

FEATURES

source

Location/Qualifiers

1. .391

/organism="Bothrops insularis"

/mol_type="mRNA"

/db_xref="taxon:8723"

/tissue type="venom glands"

/clone_lib="Snake Bothrops insularis library IL3"

/note="Organ: venom glands; Vector: pGEM11zf+; Site 1: Eco

RI; Site 2: Not I; Sug of mRNA from Bothrops insularis

venom glands were primed with oligo-(dT) and reverse

transcribed to cDNA using Superscript Plasmid System for

cDNA Synthesis and Cloning (Life Technologies). The cDNAs

were selected by size (350-600 pb and up 600 pb) in

agarose gel electrophoresis, linked to Eco RI adapters and

directionally cloned in pGEM11zf+ vector (Promega). ESTs

were generated from random clones and grouped in unique

sequences. The putative identification of each EST or

cluster was obtained through Blast searches (e-value <

e-05)."

BASE COUNT 91 a 92 c 113 g 95 t

ORIGIN

Alignment Scores:

Pred. No.: 3.28e-08 Length: 475
Score: 127.00 Matches: 20
Percent Similarity: 78.57% Conservative: 2
Best Local Similarity: 71.43% Mismatches: 6
Query Match: 74.71% Indels: 0
DB: 12 Gaps: 0

US-09-938-114-3 (1-29) x BM401469 (1-391)

QY 1 AspCysSerSerAspTrpSerSerTyrrGluGlyHisCysTyrrLysValPheLysGlnSer 20
|||||
Db 135 GATTGTCCTCTGATTGGTCCCTATGAAGGCGATTGCTACAAAGCTCTTTCAACACACGG 194

QY 21 LysThrTrpThrAspAlaGluSer 28
|||
Db 195 ATGAACCTGGCGCGATGCAGAGAAAT 218

RESULT 4

BM401621

LOCUS

DEFINITION

BM401621 Snake Bothrops insularis library IL3 Bothrops insularis

cDNA 5' similar to Snake venom C-type lectin, mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Bothrops insularis (Island jararaca)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;

Viperidae; Crotalinae; Bothrops.

REFERENCE

AUTHORS

TITLE

A survey of gene expression and diversity in the venom glands of

the pitviper snake Bothrops insularis through the generation of

expressed sequence tags (ESTs)

Gene 299 (1-2), 279-291 (2002)

JOURNAL

MEDLINE

PUBMED

COMMENT

Centro de Biotecnologia

Instituto Butantan

Av. Vital Brazil, 1500, Sao Paulo SP, BRAZIL, 05503-900

Tel: 55 11 37 26 7222 ext. 2083

Fax: 55 11 37 26 1505

Email: hoplee@usp.br

This EST corresponds to cluster BITL01A (see Reference)

Seq primer: M13F.

FEATURES

source

Location/Qualifiers

1. .475

/organism="Bothrops insularis"

/mol_type="mRNA"

/db_xref="taxon:8723"

/tissue type="venom glands"

/clone_lib="Snake Bothrops insularis library IL3"

/note="Organ: venom glands; Vector: pGEM11zf+; Site 1: Eco

RI; Site 2: Not I; Sug of mRNA from Bothrops insularis

venom glands were primed with oligo-(dT) and reverse

transcribed to cDNA using Superscript Plasmid System for

cDNA Synthesis and Cloning (Life Technologies). The cDNAs

were selected by size (350-600 pb and up 600 pb) in

agarose gel electrophoresis, linked to Eco RI adapters and

directionally cloned in pGEM11zf+ vector (Promega). ESTs

were generated from random clones and grouped in unique

sequences. The putative identification of each EST or

cluster was obtained through Blast searches (e-value <

e-05)."

BASE COUNT 113 a 111 c 133 g 117 t 1 others

ORIGIN

Alignment Scores:

Pred. No.: 4.38e-08 Length: 475
Score: 127.00 Matches: 20
Percent Similarity: 78.57% Conservative: 2
Best Local Similarity: 71.43% Mismatches: 6
Query Match: 74.71% Indels: 0
DB: 12 Gaps: 0

US-09-938-114-3 (1-29) x BM401621 (1-475)

QY 1 AspCysSerSerAspTrpSerSerTyrrGluGlyHisCysTyrrLysValPheLysGlnSer 20
|||||
Db 129 GATTGTCCTCTGATTGGTCCCTATGAAGGCGATTGCTACAAAGCTCTTTCAACACACGG 188

QY 21 LysThrTrpThrAspAlaGluSer 28
|||
Db 189 ATGAACCTGGCGCGATGCAGAGAAAT 212

RESULT 5

BM401628

LOCUS

DEFINITION

BM401628 Snake Bothrops insularis library IL3 Bothrops insularis

cDNA 5' similar to Snake venom C-type lectin, mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Bothrops insularis (Island jararaca)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;

Viperidae; Crotalinae; Bothrops.

REFERENCE

AUTHORS

TITLE

A survey of gene expression and diversity in the venom glands of

the pitviper snake Bothrops insularis through the generation of

expressed sequence tags (ESTs)

Gene 299 (1-2), 279-291 (2002)

JOURNAL

MEDLINE

PUBMED

COMMENT

Contact: Paulo Lee Ho

Centro de Biotecnologia

Instituto Butantan

Av. Vital Brazil, 1500, Sao Paulo SP, BRAZIL, 05503-900

Tel: 55 11 37 26 7222 ext. 2083
 Fax: 55 11 37 26 1505
 Email: hoplee@usp.br
 This EST corresponds to cluster BITL01A (see Reference)
 Seq primer: M13F.

FEATURES

source
 Location/Qualifiers
 1. 504

/organism="Bothrops insularis"
 /mol_type="mRNA"
 /db_xref="taxon:8723"
 /tissue_type="venom glands"
 /clone_lib="Snake Bothrops insularis library IL3"
 /note="Organ: venom glands; Vector: pGEM11zf+; Site:1: Eco RI; Site:2: Not I; Sug of mRNA from Bothrops insularis venom glands were primed with oligo-(drr) and reverse transcribed to cDNA using Superscript Plasmid System for cDNA Synthesis and Cloning (Life Technologies). The cDNAs were selected by size (350-600 pb and up 600 pb) in agarose gel electrophoresis, linked to Eco RI adapters and directionally cloned in pGEM11zf+ vector (Promega). ESTs were generated from random clones and grouped in unique sequences. The putative identification of each EST or cluster was obtained through Blast searches (e-value < e-05)."

BASE COUNT 128 a 113 c 140 g 120 t 3 others
 ORIGIN

Alignment Scores:
 Pred. No.: 4.79e-08 Length: 504
 Score: 127.00 Matches: 20
 Percent Similarity: 78.57% Conservative: 2
 Best Local Similarity: 71.43% Mismatches: 6
 Query Match: 74.71% Indels: 0
 DB: 12 Gaps: 0

US-09-938-114-3 (1-29) x BM401628 (1-504)

Qy 1 AspCysSerSerAspTrpSerSerTyGluGlyHisCysTyrlsValPheLysGlnSer 20
 Db 96 GATTGTCCCTCTGATTGGTCCCTATGAGGGCATTGCTACAGCTCTTCAACACGCG 155

Qy 21 LysThrTrpThrAspAlaGluSer 28
 Db 156 ATGAAGTGGCGGATGACAGAGAT 179

RESULT 6
 BM401667
 LOCUS
 DEFINITION J12H07F Snake Bothrops insularis library IL3 Bothrops insularis
 CDNA 5' similar to Snake venom C-type lectin, mRNA sequence.
 BM401667
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM

Bothrops insularis (island jararaca)
 Bothrops insularis
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
 Viperidae; Crotalinae; Bothrops.

REFERENCE
 AUTHORS
 TITLE
 A survey of gene expression and diversity in the venom glands of the pitviper snake Bothrops insularis through the generation of expressed sequence tags (ESTs)
 Gene 299 (1-2), 279-291 (2002)
 JOURNAL
 MEDLINE
 PUBMED
 COMMENT

Contact: Paulo Lee Ho
 Centro de Biotecnologia
 Instituto Butantan
 Av. Vital Brazil, 1500, Sao Paulo SP, BRAZIL, 05503-900
 Tel: 55 11 37 26 7222 ext. 2083
 Fax: 55 11 37 26 1505
 Email: hoplee@usp.br

This EST corresponds to cluster BITL01A (see Reference)
 Seq primer: M13F.

source
 Location/Qualifiers
 1. 510

/organism="Bothrops insularis"
 /mol_type="mRNA"
 /db_xref="taxon:8723"
 /tissue_type="venom glands"
 /clone_lib="Snake Bothrops insularis library IL3"
 /note="Organ: venom glands; Vector: pGEM11zf+; Site:1: Eco RI; Site:2: Not I; Sug of mRNA from Bothrops insularis venom glands were primed with oligo-(drr) and reverse transcribed to cDNA using Superscript Plasmid System for cDNA Synthesis and Cloning (Life Technologies). The cDNAs were selected by size (350-600 pb and up 600 pb) in agarose gel electrophoresis, linked to Eco RI adapters and directionally cloned in pGEM11zf+ vector (Promega). ESTs were generated from random clones and grouped in unique sequences. The putative identification of each EST or cluster was obtained through Blast searches (e-value < e-05)."

BASE COUNT 128 a 117 c 141 g 121 t 3 others
 ORIGIN

Alignment Scores:
 Pred. No.: 4.87e-08 Length: 510
 Score: 127.00 Matches: 20
 Percent Similarity: 78.57% Conservative: 2
 Best Local Similarity: 71.43% Mismatches: 6
 Query Match: 74.71% Indels: 0
 DB: 12 Gaps: 0

US-09-938-114-3 (1-29) x BM401667 (1-510)

Qy 1 AspCysSerSerAspTrpSerSerTyGluGlyHisCysTyrlsValPheLysGlnSer 20
 Db 93 GATTGTCCCTCTGATTGGTCCCTATGAGGGCATTGCTACAGCTCTTCAACACGCG 152

Qy 21 LysThrTrpThrAspAlaGluSer 28
 Db 153 ATGAAGTGGCGGATGACAGAGAT 176

RESULT 7
 BM401495
 LOCUS
 DEFINITION JH2B09F Snake Bothrops insularis library IL3 Bothrops insularis
 CDNA 5' similar to Snake venom C-type lectin, mRNA sequence.
 BM401495
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM

Bothrops insularis (island jararaca)
 Bothrops insularis
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
 Viperidae; Crotalinae; Bothrops.

REFERENCE
 AUTHORS
 TITLE
 A survey of gene expression and diversity in the venom glands of the pitviper snake Bothrops insularis through the generation of expressed sequence tags (ESTs)
 Gene 299 (1-2), 279-291 (2002)
 JOURNAL
 MEDLINE
 PUBMED
 COMMENT

Contact: Paulo Lee Ho
 Centro de Biotecnologia
 Instituto Butantan
 Av. Vital Brazil, 1500, Sao Paulo SP, BRAZIL, 05503-900
 Tel: 55 11 37 26 7222 ext. 2083
 Fax: 55 11 37 26 1505
 Email: hoplee@usp.br
 This EST corresponds to cluster BITL01A (see Reference)
 Seq primer: M13F.

FEATURES

Location/Qualifiers

```

source
1. .512
/organism="Bothrops insularis"
/mol_type="mRNA"
/db_xref="taxon:8723"
/clone_lib="Snake Bothrops insularis library IL3"
/notes="Organ: venom glands; Vector: pGEM11zf+; Site 1: Eco
RI; Site 2: Not I; Sug of mRNA from Bothrops insularis
venom glands were primed with oligo-(dT) and reverse
transcribed to cDNA using Superscript Plasmid System for
cDNA Synthesis and Cloning (Life Technologies). The cDNAs
were selected by size (350-600 pb and up 600 pb) in
agarose gel electrophoresis, linked to Eco RI adapters and
directionally cloned in pGEM11zf+ vector (Promega). ESTs
were generated from random clones and grouped in unique
sequences. The putative identification of each EST or
cluster was obtained through Blast searches (e-value <
e-05)."
BASE COUNT      129 a   116 c   143 g   119 t   5 others
ORIGIN
Alignment Scores:
Pred. No.:      4.9e-08      Length:      512
Score:          127.00      Matches:      20
Percent Similarity: 78.57%      Conservative: 2
Best Local Similarity: 71.43%      Mismatches: 6
Query Match:     74.71%      Indels:      0
DB:              12      Gaps:      0

US-09-938-114-3 (1-29) x BM401495 (1-512)
QY      1 AspCysSerSerAspTrpSerSerTyrGluGlyHisCysTyrLysValPheLysGlnSer 20
|||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
99  GATTGTCCTCTGATTGGTCCCTATGAGGGCATTGCTACAGCTCTTCAACACACGG 158
Db
QY      21 LysThrTrpThrAspAlaGluSer 28
|||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
159  ATGAACCTGGCGGATGCAGAGAT 192
Db

RESULT 8
BM401656
LOCUS
DEFINITION
JL2E04F Snake Bothrops insularis library IL3 Bothrops insularis
CDNA 5' similar to Snake venom C-type lectin, mRNA sequence.
ACCESSION
BM401656
VERSION
BM401656.1 GI:20376284
KEYWORDS
EST.
SOURCE
Bothrops insularis (Island Jararaca)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
Viperidae; Crotalinae; Bothrops.
REFERENCE
1 (bases 1 to 343)
Junqueira-de-Azevedo, I.L.M. and Ho, P.L.
A survey of gene expression and diversity in the venom glands of
the pitviper snake Bothrops insularis through the generation of
expressed sequence tags (ESTs)
JOURNAL
Gene 299 (1-2), 279-291 (2002)
MEDLINE
22347338
PUBMED
12459276
COMMENT
Contact: Paulo Lee Ho
Centro de Biotecnologia
Instituto Butantan
Av. Vital Brazil, 1500, Sao Paulo SP, BRAZIL, 05503-900
Tel: 55 11 37 26 7222 ext. 2083
Fax: 55 11 37 26 1505
Email: hoplee@usp.br
This EST corresponds to cluster BITL01A (see Reference)
Seq primer: M13F.
Location/Qualifiers
1. .343
/organism="Bothrops insularis"
/mol_type="mRNA"

source
1. .512
/organism="Bothrops insularis"
/mol_type="mRNA"
/db_xref="taxon:8723"
/clone_lib="Snake Bothrops insularis library IL3"
/notes="Organ: venom glands; Vector: pGEM11zf+; Site 1: Eco
RI; Site 2: Not I; Sug of mRNA from Bothrops insularis
venom glands were primed with oligo-(dT) and reverse
transcribed to cDNA using Superscript Plasmid System for
cDNA Synthesis and Cloning (Life Technologies). The cDNAs
were selected by size (350-600 pb and up 600 pb) in
agarose gel electrophoresis, linked to Eco RI adapters and
directionally cloned in pGEM11zf+ vector (Promega). ESTs
were generated from random clones and grouped in unique
sequences. The putative identification of each EST or
cluster was obtained through Blast searches (e-value <
e-05)."
BASE COUNT      79 a   83 c   90 g   86 t   5 others
ORIGIN
Alignment Scores:
Pred. No.:      1.93e-07      Length:      343
Score:          121.00      Matches:      19
Percent Similarity: 76.92%      Conservative: 1
Best Local Similarity: 73.08%      Mismatches: 6
Query Match:     71.18%      Indels:      0
DB:              12      Gaps:      0

US-09-938-114-3 (1-29) x BM401656 (1-343)
QY      1 AspCysSerSerAspTrpSerSerTyrGluGlyHisCysTyrLysValPheLysGlnSer 20
|||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
131  GATTGTCCTCTGATTGGTCCCTATGAGGGCATTGCTACAGCTCTTCAACACACGG 190
Db
QY      21 LysThrTrpThrAspAla 26
|||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
191  ATGAACCTGGCGGATGCA 208
Db

RESULT 9
BM401686
LOCUS
DEFINITION
PH015FB Snake Bothrops insularis library IL2 Bothrops insularis
CDNA 5' similar to Snake venom C-type lectin, mRNA sequence.
ACCESSION
BM401686
VERSION
BM401686.1 GI:20376314
KEYWORDS
EST.
SOURCE
Bothrops insularis (Island Jararaca)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
Viperidae; Crotalinae; Bothrops.
REFERENCE
1 (bases 1 to 633)
Junqueira-de-Azevedo, I.L.M. and Ho, P.L.
A survey of gene expression and diversity in the venom glands of
the pitviper snake Bothrops insularis through the generation of
expressed sequence tags (ESTs)
JOURNAL
Gene 299 (1-2), 279-291 (2002)
MEDLINE
22347338
PUBMED
12459276
COMMENT
Contact: Paulo Lee Ho
Centro de Biotecnologia
Instituto Butantan
Av. Vital Brazil, 1500, Sao Paulo SP, BRAZIL, 05503-900
Tel: 55 11 37 26 7222 ext. 2083
Fax: 55 11 37 26 1505
Email: hoplee@usp.br
This EST corresponds to cluster BITL02A (see Reference)
Seq primer: M13F.
Location/Qualifiers
1. .633
/organism="Bothrops insularis"
/mol_type="mRNA"
/db_xref="taxon:8723"
/tissue_type="venom glands"
/clone_lib="Snake Bothrops insularis library IL2"

```

/note="Organ: venom glands; Vector: pGEM11zf+; Site 1: Eco RI; Site 2: Not I; Sug of mRNA from Bothrops insularis venom glands were primed with oligo-(dT) and reverse transcribed to cDNA using Superscript Plasmid System for cDNA Synthesis and Cloning (Life Technologies). The cDNAs were selected by size (350-600 pb and up 600 pb) in agarose gel electrophoresis, linked to Eco RI adapters and directionally cloned in pGEM11zf+ vector (Promega). ESTs were generated from random clones and grouped in unique sequences. The putative identification of each EST or cluster was obtained through Blast searches (e-value < e-05)."

BASE COUNT 145 a 148 c 155 g 171 t 14 others
ORIGIN

Alignment Scores:
Pred. No.: 6.69e-07 Length: 633
Score: 120.00 Matches: 19
Percent Similarity: 75.00% Conservative: 2
Best Local Similarity: 67.86% Mismatches: 7
Query Match: 70.59% Indels: 0
DB: 12 Gaps: 0

US-09-938-114-3 (1-29) x BM401686 (1-633)

Qy 1 AspCysSerSerAspTrpSerSerTyrrGluGlyHisCysTyrrLysValPheLysGlnSer 20
|||||
Db 82 GATTGTCCCTCTGATTGGTCCCTCTATGGAGGCAATTGCTACAGCTCTTCAACACGG 141
|||||
Qy 21 LysThrTrpThrAspAlaGluSer 28
|||||
Db 142 ATGAACCTGGCGGATGCAGAGAT 165
|||||

RESULT 10
BM401620
LOCUS BM401620 378 bp mRNA linear EST 01-MAY-2002
DEFINITION J141C11F Snake Bothrops insularis library IL3 Bothrops insularis
cDNA 5' similar to Snake venom C-type lectin, mRNA sequence.

ACCESSION BM401620.1 GI:20376248
VERSION BM401620.1
KEYWORDS EST.
SOURCE Bothrops insularis (island jararaca)

ORGANISM Bothrops insularis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
Viperidae; Crotalinae; Bothrops.

REFERENCE 1 (bases 1 to 378)
AUTHORS Junqueira-de-Azevedo, I.L.M. and Ho, P.L.
TITLE A survey of gene expression and diversity in the venom glands of the pitviper snake Bothrops insularis through the generation of expressed sequence tags (ESTs)

JOURNAL Gene 299 (1-2), 279-291 (2002)
MEDLINE 22347338
PUBMED 12459276
COMMENT Contact: Paulo Lee Ho
Centro de Biotecnologia
Instituto Butantan
Av. Vital Brazil, 1500, Sao Paulo SP, BRAZIL, 05503-900
Tel: 55 11 37 26 7222 ext. 2083
Fax: 55 11 37 26 1505
Email: hoplee@usp.br
This EST corresponds to cluster BIT11A (see Reference)
Seq primer: M13F.

FEATURES
source
1..378
Location/Qualifiers
/organism="Bothrops insularis"
/mol_type="mRNA"
/db_xref="taxon:8723"
/tissue_type="venom glands"
/clone_lib="Snake Bothrops insularis library IL3"

/note="Organ: venom glands; Vector: pGEM11zf+; Site 1: Eco RI; Site 2: Not I; Sug of mRNA from Bothrops insularis venom glands were primed with oligo-(dT) and reverse

transcribed to cDNA using Superscript Plasmid System for cDNA Synthesis and Cloning (Life Technologies). The cDNAs were selected by size (350-600 pb and up 600 pb) in agarose gel electrophoresis, linked to Eco RI adapters and directionally cloned in pGEM11zf+ vector (Promega). ESTs were generated from random clones and grouped in unique sequences. The putative identification of each EST or cluster was obtained through Blast searches (e-value < e-05)."

BASE COUNT 82 a 105 c 99 g 92 t
ORIGIN

Alignment Scores:
Pred. No.: 4.31e-07 Length: 378
Score: 119.00 Matches: 19
Percent Similarity: 72.41% Conservative: 2
Best Local Similarity: 65.52% Mismatches: 8
Query Match: 70.00% Indels: 0
DB: 12 Gaps: 0

US-09-938-114-3 (1-29) x BM401620 (1-378)

Qy 1 AspCysSerSerAspTrpSerSerTyrrGluGlyHisCysTyrrLysValPheLysGlnSer 20
|||||
Db 149 GATTGTCCCTCTGATTGGTCCCTCTATGAAGGAGTTGCTACAGGCTCTTCGAACAAAAG 208
|||||
Qy 21 LysThrTrpThrAspAlaGluSerPhe 29
|||||
Db 209 ATGAACCTGGGAGGATGCAGAGAAATTC 235
|||||

RESULT 11
BM401417

LOCUS BM401417 574 bp mRNA linear EST 01-MAY-2002
DEFINITION GH061F Snake Bothrops insularis library IL2 Bothrops insularis cDNA
5' similar to Snake venom C-type lectin, mRNA sequence.

ACCESSION BM401417.1 GI:20376045
VERSION BM401417
KEYWORDS EST.
SOURCE Bothrops insularis (island jararaca)

ORGANISM Bothrops insularis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
Viperidae; Crotalinae; Bothrops.

REFERENCE 1 (bases 1 to 574)
AUTHORS Junqueira-de-Azevedo, I.L.M. and Ho, P.L.
TITLE A survey of gene expression and diversity in the venom glands of the pitviper snake Bothrops insularis through the generation of expressed sequence tags (ESTs)

JOURNAL Gene 299 (1-2), 279-291 (2002)
MEDLINE 22347338
PUBMED 12459276
COMMENT Contact: Paulo Lee Ho
Centro de Biotecnologia
Instituto Butantan
Av. Vital Brazil, 1500, Sao Paulo SP, BRAZIL, 05503-900
Tel: 55 11 37 26 7222 ext. 2083
Fax: 55 11 37 26 1505
Email: hoplee@usp.br
This EST corresponds to cluster BIT10A (see Reference)
Seq primer: M13F.

FEATURES
source
1..574
Location/Qualifiers
/organism="Bothrops insularis"
/mol_type="mRNA"
/db_xref="taxon:8723"
/tissue_type="venom glands"

/clone_lib="Snake Bothrops insularis library IL2"
/note="Organ: venom glands; Vector: pGEM11zf+; Site 1: Eco RI; Site 2: Not I; Sug of mRNA from Bothrops insularis venom glands were primed with oligo-(dT) and reverse transcribed to cDNA using Superscript Plasmid System for cDNA Synthesis and Cloning (Life Technologies). The cDNAs were selected by size (350-600 pb and up 600 pb) in


```

BASE COUNT      63 a      78 c      86 g      74 t
ORIGIN

Alignment Scores:
Pred. No.:      5.92e-07      Length:      301
Score:          117.00      Matches:      19
Percent Similarity: 78.57%      Conservative: 3
Best Local Similarity: 67.86%      Mismatches: 6
Query Match:     68.82%      Indels:      0
DB:             12      Gaps:      0

US-09-938-114-3 (1-29) x BM401654 (1-301)

QY 2 CysSerSerAspTrpSerTyrGluGlyHisCysTyrLysValPheLysGlnSerLys 21
   |||
Db 87 TGTCCCTTGGGTGGTCTCTCTATGATGAGCAATGCTACAGGGTCTTCAAGGAACCTCAA 146
   |||

QY 22 ThrTrpThrAspAlaGluSerPhe 29
   |||
Db 147 ACCTGGATGATGCAGAGAGTTTC 170
   |||

RESULT 14
BM401460
LOCUS
DEFINITION
  JH1D06F Snake Bothrops insularis library IL3 Bothrops insularis
  cDNA 5' similar to Snake venom C-type lectin, mRNA sequence.
ACCESSION
  BM401460
VERSION
  BM401460.1 GI:20376088
KEYWORDS
  EST.
SOURCE
  Bothrops insularis (island jararaca)
ORGANISM
  Bothrops insularis
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
  Viperidae; Crotalinae; Bothrops.
REFERENCE
  1 (bases 1 to 460)
  Junqueira-de-Azevedo, I.L.M. and Ho, P.L.
  A survey of gene expression and diversity in the venom glands of
  the pitviper snake Bothrops insularis through the generation of
  expressed sequence tags (ESTs)
  Gene 299 (1-2), 279-291 (2002)
JOURNAL
  MEDLINE
  PUBMED
  12459276
COMMENT
  Contact: Paulo Lee Ho
  Instituto Butantan
  Av. Vital Brazil, 1500, Sao Paulo SP, BRAZIL, 05503-900
  Tel: 55 11 37 26 7222 ext. 2083
  Fax: 55 11 37 26 1505
  Email: hoplee@usp.br
  This EST corresponds to cluster BITL13A (see Reference)
  Seq primer: M13P.
  Location/Qualifiers
    source
      1..460
        /organism="Bothrops insularis"
        /mol_type="mRNA"
        /db_xref="taxon:8723"
        /tissue_type="venom glands"
        /clone_lib="Snake Bothrops insularis library IL3"
        /note="Organ: venom glands; Vector: pGEM11zf+; Site 1: Eco
  RI; Site 2: Not I; Sug of mRNA from Bothrops insularis
  venom glands were primed with oligo-(dT) and reverse
  transcribed to cDNA using Superscript Plasmid System for
  cDNA Synthesis and Cloning (Life Technologies). The cDNAs
  were selected by size (350-600 pb and up 600 pb) in
  agarose gel electrophoresis, linked to Eco RI adapters and
  directionally cloned in pGEM11zf+ vector (Promega). ESTs
  were generated from random clones and grouped in unique
  sequences. The putative identification of each EST or
  cluster was obtained through Blast searches (e-value <
  e-05)."

BASE COUNT      106 a      106 c      145 g      103 t
ORIGIN

Alignment Scores:
Pred. No.:      4.22e-06      Length:      374
Score:          115.00      Matches:      18
Percent Similarity: 72.41%      Conservative: 3
Best Local Similarity: 62.07%      Mismatches: 8
Query Match:     67.65%      Indels:      0
DB:             12      Gaps:      0

US-09-938-114-3 (1-29) x BM401460 (1-460)

QY 1 AspCysSerSerAspTrpSerTyrGluGlyHisCysTyrLysValPheLysGlnSer 20
   |||
Db 143 GATGTCCCTTGGTGGTCTCTCTATGAGGAGTGTCTACAGGGTCTTCACTGAACCG 202
   |||

QY 21 LysThrTrpThrAspAlaGluSerPhe 29
   |||
Db 203 CAAACTGGGCCGATGCAGAGAGTTTC 229
   |||

RESULT 15
BM401520
LOCUS
DEFINITION
  JH2G02F Snake Bothrops insularis library IL3 Bothrops insularis
  cDNA 5' similar to Snake venom C-type lectin, mRNA sequence.
ACCESSION
  BM401520
VERSION
  BM401520.1 GI:20376148
KEYWORDS
  EST.
SOURCE
  Bothrops insularis (island jararaca)
ORGANISM
  Bothrops insularis
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
  Viperidae; Crotalinae; Bothrops.
REFERENCE
  1 (bases 1 to 374)
  Junqueira-de-Azevedo, I.L.M. and Ho, P.L.
  A survey of gene expression and diversity in the venom glands of
  the pitviper snake Bothrops insularis through the generation of
  expressed sequence tags (ESTs)
  Gene 299 (1-2), 279-291 (2002)
JOURNAL
  MEDLINE
  PUBMED
  12459276
COMMENT
  Contact: Paulo Lee Ho
  Centro de Biotecnologia
  Instituto Butantan
  Av. Vital Brazil, 1500, Sao Paulo SP, BRAZIL, 05503-900
  Tel: 55 11 37 26 7222 ext. 2083
  Fax: 55 11 37 26 1505
  Email: hoplee@usp.br
  This EST corresponds to cluster BITL06A (see Reference)
  Seq primer: M13P.
  Location/Qualifiers
    source
      1..374
        /organism="Bothrops insularis"
        /mol_type="mRNA"
        /db_xref="taxon:8723"
        /tissue_type="venom glands"
        /clone_lib="Snake Bothrops insularis library IL3"
        /note="Organ: venom glands; Vector: pGEM11zf+; Site 1: Eco
  RI; Site 2: Not I; Sug of mRNA from Bothrops insularis
  venom glands were primed with oligo-(dT) and reverse
  transcribed to cDNA using Superscript Plasmid System for
  cDNA Synthesis and Cloning (Life Technologies). The cDNAs
  were selected by size (350-600 pb and up 600 pb) in
  agarose gel electrophoresis, linked to Eco RI adapters and
  directionally cloned in pGEM11zf+ vector (Promega). ESTs
  were generated from random clones and grouped in unique
  sequences. The putative identification of each EST or
  cluster was obtained through Blast searches (e-value <
  e-05)."

BASE COUNT      83 a      83 c      114 g      94 t
ORIGIN

Alignment Scores:
Pred. No.:      4.22e-06      Length:      374
Score:          112.00      Matches:      18

```

Percent Similarity: 74.07% Conservative: 2
Best Local Similarity: 66.67% Mismatches: 7
Query Match: 65.88% Indels: 0
DB: 12 Gaps: 0

US-09-938-114-3 (1-29) x BM401520 (1-374)

QY 1 AspCysSerSerAspTyrSerSerTyGluGlyHisCysTyrLysValPheLysGlnSer 20
Db 130 GATTGTCCTCCCTGATTGGTCTCTATGAGGGAGTTGCTACAAGCTCTTCAGACAAGAG 189
QY 21 LysThrTyrThrAspAlaGlu 27
Db 190 TTGAAGTGGGAGGATGCAGAG 210

Search completed: December 8, 2003, 17:24:33
Job time : 754.514 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 8, 2003, 09:45:44 ; Search time 10.2 Seconds
(without alignments)
264.544 Million cell updates/sec

Title: US-09-938-114-4

Perfect score: 108

Sequence: 1 DCPSEWSYRGFCVKPF 17

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A_Geneseq_19Jun03.*
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24: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	101	93.5	146	24	ABU08799
2	95	88.0	120	23	ABE83143
3	94	87.0	30	22	AAM51540
4	94	87.0	146	22	AAM51544
5	86	79.6	21	16	AA71980
6	86	79.6	28	13	AAK23886
7	86	79.6	116	13	AAK24427
8	86	79.6	123	14	AAK38225
9	84	77.8	30	16	AA72232

10	84	77.8	32	16	AA72231	Vipera palestinae
11	84	77.8	43	16	AA72234	Vipera palestinae
12	84	77.8	50	13	AAK23889	N-terminal sequenc
13	84	77.8	52	16	AA72233	Vipera palestinae
14	84	77.8	127	16	AA72236	Vipera palestinae
15	84	77.8	132	16	AA72235	Vipera palestinae
16	84	77.8	145	23	AAO14521	Korean adder snake
17	83	76.9	36	13	AAK23885	N-terminal sequenc
18	83	76.9	38	16	AA71978	Snake venom derive
19	83	76.9	110	23	AAO20975	110-mer central lo
20	83	76.9	126	16	AA71979	Snake venom derive
21	83	76.9	126	21	AA785627	Snake venom derive
22	83	76.9	126	23	AAO20973	126-mer wild-type
23	83	76.9	126	23	AAO20980	M7-G4 K20A mutant
24	83	76.9	126	23	AAO20981	M8-G4 D54A mutant
25	83	76.9	126	23	AAO20982	M9-G4 Y58A mutant
26	83	76.9	126	23	AAO20983	M10-G4 K61A mutant
27	83	76.9	126	23	AAO20984	M11-G4 E62A mutant
28	83	76.9	126	23	AAO20985	M12-G4 Y63A mutant
29	83	76.9	126	23	AAO20986	M13-G4 R66A mutant
30	83	76.9	126	23	AAO20987	M14-G4 Y67A mutant
31	83	76.9	126	23	AAO20988	M15-G4 R100A mutant
32	83	76.9	126	23	AAO20989	M16-G4 D101A mutant
33	83	76.9	126	23	AAO20990	M17-G4 R103A mutant
34	83	76.9	126	23	AAO20991	M18-G4 R105A mutant
35	83	76.9	126	23	AAO20992	M19-G4 E106A mutant
36	83	76.9	126	23	AAO20993	M20-G4 F108A mutant
37	83	76.9	126	23	AAO20994	M21-G4 D54A, D101N
38	83	76.9	126	23	AAO20995	M22-G4 D54A, D101A
39	83	76.9	126	23	AAO20996	M23-G4 D54N, D101A
40	83	76.9	126	23	AAO20997	M24-G4 D54A, D101A
41	83	76.9	126	23	AAO20998	M25-G4 D101A, E106
42	83	76.9	126	23	AAO20999	M26-G4 D101A, E106
43	83	76.9	127	13	AAK24426	Sequence of the pl
44	83	76.9	149	16	AA71981	Snake venom antith
45	83	76.9	149	21	AA785628	Snake venom derive

ALIGNMENTS

RESULT 1

ABU08799
ID ABU08799 standard; Protein; 146 AA.

XX ABU08799;

XX AC

XX 02-JUN-2003 (first entry)

DE Deinagkistrodon acutus antithrombosis enzyme beta chain.

XX Antithrombosis; beta chain; fibrin hydrolysis; blood clot; enzyme;
XX platelet aggregation; vaso-occlusive disorder; thromboembolic disorder;
XX myocardial infarction; restenosis; cancer; neurodegenerative disease;
XX angiothrombosis; cerebral thrombosis; thromboangiitis obliterans;
XX ischaemic cerebral vascular disease; unstable angina; acute thrombosis;
XX unstable stenocardia; pulmonary embolism; deep vein thrombosis; oedema;
XX peripheral arterial occlusion; stroke; atherosclerosis; inflammation;
XX thrombosis.

OS Deinagkistrodon acutus.

Key	Location/Qualifiers
Peptide	1..23
Protein	/note= "Leader peptide"
	24..146
	/note= "Mature antithrombosis enzyme beta chain. Residues 24 to 40 specifically claimed in claim 8"
Misc-difference	72
	/label= Unknown
Misc-difference	72
	/note= "Encoded by TNN"
	/label= Unknown

FT Misc-difference 72 /note= "Encoded by NNN"
 FT 72 /label= Unknown
 FT /note= "Encoded by NNN"
 FT Misc-difference 72
 FT 72 /label= Unknown
 FT /note= "Encoded by NNT"
 XX
 PN US6489451-B1.
 XX
 XX 03-DEC-2002.
 XX
 XX 10-APR-1998; 98US-0058740.
 XX
 XX 10-APR-1997; 97US-043886P.
 XX (HEFE-) HEFEI SIU FUNG USFC PHARM CO LTD.
 XX
 XX Li BX, Cheng X;
 XX
 XX WPI; 2003-352116/33.
 DR N-PSDB; ABX93674.
 XX
 XX New purified Agkistrodon actus anti-thrombosis enzyme, useful for
 PT preventing and treating vaso-occlusive and thromboembolic disorders,
 PT including myocardial infarction, restenosis, cerebral thrombosis and
 PT unstable angina
 XX
 XX Disclosure; Fig 1; 19pp; English.
 XX
 XX The invention relates to a new Deinagkistrodon actus anti-thrombosis
 CC enzyme, where the enzyme hydrolyses fibrin, dissolves blood clots and
 CC prevents platelet aggregation. The anti-thrombosis enzyme was
 CC administered to rabbits intravenously. Thrombosis was determined before
 CC and after the administration at 0.5, 1.0, 2.0 and 3.0 hours by the
 CC Chandler method. The enzyme showed anti-thrombosis activity at 0.5 hour
 CC following administration at 0.005 micro/kg and this activity was
 CC increased significantly at 1.0 hour and at 0.01 micro /kg. The
 CC composition is useful for preventing and treating vaso-occlusive and
 CC thromboembolic disorders, including myocardial infarction, restenosis,
 CC angioathic thrombosis, cerebral thrombosis, ischaemic cerebral vascular
 CC diseases, unstable angina, acute thrombosis, unstable stenocardia,
 CC thromboangiitis obliterans, pulmonary embolism, deep vein thrombosis,
 CC peripheral arterial occlusion, stroke. It is also useful for treating
 CC atherosclerosis, oedema and inflammation, cancer and neurodegenerative
 CC diseases. The present sequence represents the amino acid sequence of the
 CC Deinagkistrodon actus antithrombosis enzyme beta chain.
 XX
 XX Sequence 146 AA;
 SQ
 Query Match 93.5%; Score 101; DB 24; Length 146;
 Best Local Similarity 94.1%; Pred. NO. 2.2e-06;
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 DCPSEWSYEGFCYKPF 17
 Db 24 DCPSEWSYEGFCYKPF 40
 RESULT 2
 ABB83143
 ID ABB83143 standard; protein; 120 AA.
 XX
 XX ABB83143;
 AC
 XX
 XX 06-AUG-2002 (first entry)
 DT
 DE Ahylysantinfarctase thrombase II subunit B.
 XX
 XX Ahylysantinfarctase thrombase II subunit B; snake; venom;
 KW Chinese Agkistrodon acutus; purification.
 XX
 XX Agkistrodon acutus.
 OS

XX
 PN CNI332242-A.
 XX
 XX 23-JAN-2002.
 PD
 XX
 XX 29-APR-2001; 2001CN-0115570.
 PF
 XX
 XX 29-APR-2001; 2001CN-0115570.
 PR
 XX (KUNM-) KUNMING ZOOLOGY INST CHINESE ACAD SCI.
 PA
 XX Xiao C;
 XX
 XX WPI; 2002-281833/33.
 DR
 XX
 XX Ahylysantinfarctase thrombase and its production process -
 PT
 XX
 XX Claim 4; Page 5 (Disclosure); 8pp; Chinese.
 PS
 XX
 XX The present invention relates to a method for purifying
 CC Ahylysantinfarctase thrombase II from the snake venom of Chinese
 CC Agkistrodon acutus. The method involves using an anionic exchange column
 CC chromatographic process to separate and purify and the repurifying the
 CC thrombase in a fast protein purifying work station. It was found that the
 CC Ahylysantinfarctase thrombase II consists of two subunits, Subunit A
 CC (ABB83142) and Subunit B (the present sequence).
 CC
 XX Sequence 120 AA;
 SQ
 Query Match 88.0%; Score 95; DB 23; Length 120;
 Best Local Similarity 82.4%; Pred. No. 1.2e-05;
 Matches 14; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 DCPSEWSYEGFCYKPF 17
 Db 1 DCPSEWSYEGFCYKPF 17
 RESULT 3
 AAM51540
 ID AAM51540 standard; peptide; 30 AA.
 XX
 XX AAM51540;
 AC
 XX
 XX 10-JAN-2002 (first entry)
 DT
 XX
 XX Snake venom blood anticoagulant peptide #1.
 DE
 XX
 XX Snake; pit viper; venom; halyxin; anticoagulant; thrombogenesis;
 KW thrombosis.
 KW
 OS Agkistrodon halyx.
 XX
 XX KR2001049671-A.
 PN
 XX
 XX 15-JUN-2001.
 PD
 XX
 XX 29-JUN-2000; 2000KR-0036591.
 PF
 XX
 XX 29-JUN-1999; 99KR-0025105.
 PR
 XX (BIOB-) BIOBUD CO LTD.
 PA
 XX Jang YS, Jung GH, Kim DS, Koo BH, Son YD;
 PI
 XX WPI; 2001-637330/73.
 DR
 XX
 XX Halyxin as blood anticoagulation protein separated from snake venom -
 PT
 XX
 XX Example 1; Page 8; 21pp; Korean.
 PS
 XX The invention relates to halyxin, a novel protein with very strong
 CC blood anticoagulation activity. The protein was separated from snake

CC venom of Agkistrodon halys brevicaudus (a Korean pit viper) and can
 CC be used in the treatment of thrombogenesis. The present sequence is
 CC a peptide derived from the protein.

SQ Sequence 30 AA;

Query Match 87.0%; Score 94; DB 22; Length 30;

Best Local Similarity 88.2%; Pred. No. 4.9e-06;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 DCPSEWSSYEGFCYKPF 17

Db 1 DCPSGWSSYEGHCYKPF 17

RESULT 4

AA51544
 ID AAM51544 standard; Protein; 146 AA.

AC AAM51544;

DT 10-JAN-2002 (first entry)

DE Snake venom blood anticoagulant halyxin B chain.

XX Snake; pit viper; venom; halyxin; anticoagulant; thrombogenesis;
 KW thrombosis.

OS Agkistrodon halys.

XX KR2001049671-A.

XX 15-JUN-2001.

PF 29-JUN-2000; 2000KR-0036591.

XX 29-JUN-1999; 99KR-0025105.

XX (BIOB-) BIOUD CO LTD.

PI Jang YS, Jung GH, Kim DS, Koo BH, Son YD;

XX WPI; 2001-637330/73.

DR N-PSDB; AAI71877.

XX Halyxin as blood anticoagulation protein separated from snake venom -

PS Claim 2; Page 11-12; 21pp; Korean.

XX The invention relates to halyxin, a novel protein with very strong
 CC blood anticoagulation activity. The protein was separated from snake
 CC venom of Agkistrodon halys brevicaudus (a Korean pit viper) and can
 CC be used in the treatment of thrombogenesis. The present sequence
 CC is the B chain of halyxin.

XX SQ Sequence 146 AA;

Query Match 87.0%; Score 94; DB 22; Length 146;

Best Local Similarity 88.2%; Pred. No. 2e-05;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 DCPSEWSSYEGFCYKPF 17

Db 24 DCPSGWSSYEGHCYKPF 40

RESULT 5

AA71980

ID AAR71980 standard; peptide; 21 AA.

AC AAR71980;

XX 25-MAR-2003 (updated)

DT 28-NOV-1995 (first entry)
 XX Snake venom derived antithrombotic peptide.
 DE Antithrombotic peptide; snake venom; platelet binding inhibition;
 XX von Willebrand factors; Crotales horridus horridus.
 KW Crotales horridus horridus.

OS WO9508573-A1.

XX 30-MAR-1995.

XX 21-SEP-1994; 94WO-JP01555.

XX 22-SEP-1993; 93JP-0236975.

XX (AJIN) AJINOMOTO KK.

XX Fukuchi N, Ishii K, Kito M, Kobayashi T, Nagano M;

XX Tanaka A, Yamamoto H, Yoshimoto R;

XX WPI; 1995-139559/18.

XX Single-chain antithrombotic peptide - obtained by cleaving an
 PT oligopeptide from snake venom to break inter-chain di:sulphide
 PT bonds but preserve intra-chain di:sulphide bonds

XX Example 2; Page 45; 84pp; Japanese.

XX AAR71980 is a snake venom derived antithrombotic peptide, prepared
 CC by cleaving the interpeptide but retaining the intrapeptide
 CC disulphide bonds of the original snake venom oligopeptide. The
 CC peptide has the advantage of avoiding significant thrombocytopenia
 CC when administered at the minimum dose, for in vivo inhibition of
 CC platelet von Willebrand factor binding.
 CC (Updated on 25-MAR-2003 to correct PN field.)

XX SQ Sequence 21 AA;

Query Match 79.6%; Score 86; DB 16; Length 21;

Best Local Similarity 76.5%; Pred. No. 4.4e-05;
 Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 DCPSEWSSYEGFCYKPF 17

Db 1 DCPDWSYEGHCYRVF 17

RESULT 6

AA23886

ID AAR23886 standard; Protein; 28 AA.

XX AAR23886;

XX 25-MAR-2003 (updated)

DT 21-NOV-1992 (first entry)

XX N-terminal sequence of the earlier eluting subunit (CHH-B-beta) of
 DE the later eluting peak of the platelet antiadhesive peptide (PAA).

XX Platelet adherence inhibitor; platelet anti-adhesive;
 KW antithrombotic agent; von Willebrand Factor;
 KW platelet glycoprotein GPIb-IX complex.

XX Crotales horridus horridus.

XX WO9208472-A1.

XX 29-MAY-1992.

XX 14-NOV-1991; 91WO-US08516.

PR 16-NOV-1990; 90US-0614443.
 XX (CORT-) COR THERAPEUTICS INC.
 XX Scarborough RM;
 XX WPI; 1992-199936/24.
 XX Platelet antiadhesive peptide(s) obtd. from snake venom - also
 PT inhibit thrombus formation; for treatment of arteriosclerosis,
 PT atherosclerosis, acute myocardial infarction, chronic unstable
 PT angina, etc.
 XX Claim 4; Page 30; 5pp; English.
 PS
 XX The PAA was purified from a solution of snake venom. Analysis of
 CC the peak inhibitory fractions by SDS-PAGE revealed 2 major proteins
 CC migrating with a mol. wt. 23-28 kD. Both were able to inhibit
 CC botrocetin and ristocetin induced platelet agglutination. They were
 CC called CHH-A and CHH-B. The earlier eluting subunit (CHH-B-beta)
 CC and later eluting subunit (CHH-B-alpha) were individually submitted
 CC to N-terminal sequence analysis. The complete amino acid sequence
 CC for the alpha and beta chains are given in AAR24426 and AAR24427.
 CC (Updated on 25-MAR-2003 to correct PN field.)
 XX
 XX Sequence 28 AA;
 PS Query Match 79.6%; Score 86; DB 13; Length 28;
 XX Best Local Similarity 76.5%; Pred. No. 5.7e-05;
 XX Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 QY 1 DCPSEWSSYEGFCYKPF 17
 DB 1 DCPSDWSSYEGHCYRVF 17
 RESULT 7
 AAR24427
 ID AAR24427 standard; Protein; 116 AA.
 XX AC AAR24427;
 XX 25-MAR-2003 (updated)
 DT 21-NOV-1992 (first entry)
 XX Sequence of the platelet glycoprotein GPIb inhibitor beta chain
 DE (CHH-B-beta).
 XX Platelet adherence inhibitor; platelet anti-adhesive;
 KW antithrombotic agent; von Willebrand Factor;
 KW platelet glycoprotein GPIb-IX complex.
 XX Crotalus horridus horridus.
 OS
 XX WO9208472-A1.
 XX 29-MAY-1992.
 XX 14-NOV-1991; 91WO-US08516.
 XX 16-NOV-1990; 90US-0614443.
 XX (CORT-) COR THERAPEUTICS INC.
 XX Scarborough RM;
 XX WPI; 1992-199936/24.
 XX Platelet antiadhesive peptide(s) obtd. from snake venom - also
 XX inhibit thrombus formation; for treatment of arteriosclerosis,
 XX atherosclerosis, acute myocardial infarction, chronic unstable
 XX angina, etc.
 XX Example; Fig 6; 5pp; English.

XX The PAA was purified from a solution of snake venom. Analysis of
 CC the peak inhibitory fractions by SDS-PAGE revealed 2 major proteins
 CC migrating with a mol. wt. 23-28 kD. Both were able to inhibit
 CC botrocetin and ristocetin induced platelet agglutination. They were
 CC called CHH-A and CHH-B. The earlier eluting subunit (CHH-B-beta)
 CC and later eluting subunit (CHH-B-alpha) were individually submitted
 CC to N-terminal sequence analysis. The complete amino acid sequence
 CC for the alpha and beta chains are given in AAR24426 and AAR24427.
 CC (Updated on 25-MAR-2003 to correct PN field.)
 XX
 XX Sequence 116 AA;
 PS Query Match 79.6%; Score 86; DB 13; Length 116;
 XX Best Local Similarity 76.5%; Pred. No. 0.00021;
 XX Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 QY 1 DCPSEWSSYEGFCYKPF 17
 DB 1 DCPSDWSSYEGHCYRVF 17
 RESULT 8
 AAR38225
 ID AAR38225 standard; protein; 123 AA.
 XX AC AAR38225;
 XX 25-MAR-2003 (updated)
 DT 01-OCT-1993 (first entry)
 XX Sequence of polypeptide chain of albosagregin A (AL-A).
 DE Venom; snake; platelet-binding protein.
 XX Trimeresurus albolabris.
 OS
 XX WO9311151-A1.
 XX 10-JUN-1993.
 XX 01-DEC-1992; 92WO-US10344.
 XX 03-DEC-1991; 91US-0803630.
 XX 05-JUN-1992; 92US-0893929.
 XX (UTEM) UNIV TEMPLE.
 XX Kirby EP, Peng M;
 XX WPI; 1993-196991/24.
 XX New platelet-binding proteins obtained from snake venom - inhibit
 PT binding of von Willebrand factor to platelet membrane
 PT glycoprotein IB, useful in therapy, diagnosis and surgery
 XX Claim 4; Page 47; 74pp; English.
 PS
 XX AL-A may be obtd. from snake venom. It has a mol. wt. of about 45
 CC kDa. AL-A contains two types of polypeptide chains, with mol. wt. of
 CC about 18 kDa and about 15 kDa, respectively. Each of these two types
 CC of chains is actually composed of two subtypes. Thus, AL-A comprises
 CC four non-identical polypeptide chains. A possible variation of
 CC AAR38224 has been found, characterised by Asp at posn. three in lieu
 CC of Cys.
 CC (Updated on 25-MAR-2003 to correct PN field.)
 XX
 XX Sequence 123 AA;
 PS Query Match 79.6%; Score 86; DB 14; Length 123;
 XX Best Local Similarity 76.5%; Pred. No. 0.00022;
 XX Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 DCPSEWSSYEGFCYKPF 17
 ||||:|||||
 Db 1 DCPSDWSSYEGHCYKVP 17

RESULT 9
 AAR72232
 ID AAR72232 standard; peptide; 30 AA.

XX AC AAR72232;
 XX XX 25-MAR-2003 (updated)
 DT 04-DEC-1995 (first entry)
 XX XX Vipera palestinae venom derived peptide N-terminal fragment.

XX KW Vipera palestinae; venom; N-terminal fragment; antithrombotic agent;
 KW platelet binding; von Willebrand factor.

XX OS Vipera palestinae.
 XX PN WO9509183-A1.
 XX PD 06-APR-1995.

XX PF 27-SEP-1994; 94WO-JP01583.
 XX PR 28-SEP-1993; 93JP-0241666.
 PR 14-JAN-1994; 94JP-0002691.
 PR 10-JUN-1994; 94JP-0128518.

XX PA (AJIN) AJINOMOTO KK.

XX PI Fukuchi N, Ishii K, Kaide K, Kobayashi T;

XX DR WPI; 1995-147392/19.

XX PT Peptide derived from Vipera palestinae venom - inhibits binding
 PT of platelets to von Willebrand factor, useful as antithrombotic
 PT agent

XX PS Claim 3; Page 17; 37pp; Japanese.

XX CC AAR72232 is a Vipera palestinae venom derived N-terminal fragment,
 CC the full peptide is given in AAR72236. A peptide compsn. comprising
 CC AAR72236 and AAR72235 is claimed, it inhibits the binding of platelets
 CC to von Willebrand factors and can therefore be used as an anti-
 CC thrombotic agent.
 CC (Updated on 25-MAR-2003 to correct PN field.)

XX SQ Sequence 30 AA;

Query Match 77.8%; Score 84; DB 16; Length 30;
 Best Local Similarity 76.5%; Pred. No. 0.00011;
 Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 DCPSEWSSYEGFCYKPF 17
 ||||:|||||
 Db 1 DCPSDWSSYEGHCYKVP 17

RESULT 10
 AAR72231
 ID AAR72231 standard; peptide; 32 AA.

XX AC AAR72231;

XX XX 25-MAR-2003 (updated)
 DT 04-DEC-1995 (first entry)

XX DE Vipera palestinae venom derived peptide N-terminal fragment.

XX KW Vipera palestinae; venom; N-terminal fragment; antithrombotic agent;

KW platelet binding; von Willebrand factor.

XX Vipera palestinae.

XX OS WO9509183-A1.

XX PN 06-APR-1995.

XX PD 27-SEP-1994; 94WO-JP01583.

XX PR 28-SEP-1993; 93JP-0241666.

PR 14-JAN-1994; 94JP-0002691.

PR 10-JUN-1994; 94JP-0128518.

XX PA (AJIN) AJINOMOTO KK.

XX PI Fukuchi N, Ishii K, Kaide K, Kobayashi T;

XX DR WPI; 1995-147392/19.

XX PT Peptide derived from Vipera palestinae venom - inhibits binding
 PT of platelets to von Willebrand factor, useful as antithrombotic
 PT agent

XX PS Claim 3; Page 17; 37pp; Japanese.

XX CC AAR72231 is a Vipera palestinae venom derived N-terminal fragment,
 CC the full peptide is given in AAR72235. A peptide compsn. comprising
 CC AAR72235 and AAR72236 is claimed, it inhibits the binding of platelets
 CC to von Willebrand factors and can therefore be used as an anti-
 CC thrombotic agent.
 CC (Updated on 25-MAR-2003 to correct PN field.)

XX SQ Sequence 32 AA;

Query Match 77.8%; Score 84; DB 16; Length 32;
 Best Local Similarity 76.5%; Pred. No. 0.00012;
 Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 DCPSEWSSYEGFCYKPF 17
 ||||:|||||
 Db 3 DCPSDWSSYEGHCYKVP 19

RESULT 11
 AAR72234

ID AAR72234 standard; peptide; 43 AA.

XX AC AAR72234;

XX DT 25-MAR-2003 (updated)

DT 04-DEC-1995 (first entry)

XX DE Vipera palestinae venom derived peptide N-terminal fragment.

XX KW Vipera palestinae; venom; N-terminal fragment; antithrombotic agent;
 KW platelet binding; von Willebrand factor.

XX OS Vipera palestinae.

XX PN WO9509183-A1.

XX PD 06-APR-1995.

XX PF 27-SEP-1994; 94WO-JP01583.

XX PR 28-SEP-1993; 93JP-0241666.

PR 14-JAN-1994; 94JP-0002691.

PR 10-JUN-1994; 94JP-0128518.

XX PA (AJIN) AJINOMOTO KK.

XX PI Fukuchi N, Ishii K, Kaide K, Kobayashi T;

XX
DR WPI; 1995-147392/19.
XX
PT Peptide derived from Vipera palestinae venom - inhibits binding
PT of platelets to von Willebrand factor, useful as antithrombotic
PT agent
XX
PS Claim 4; Page 18; 37pp; Japanese.
XX
CC AAR72234 is a Vipera palestinae venom derived N-terminal fragment,
CC the full peptide is given in AAR72236. A peptide compsn. comprising
CC AAR72236 and AAR72235 is claimed, it inhibits the binding of platelets
CC to von Willebrand factors and can therefore be used as an anti-
CC thrombotic agent.
CC (Updated on 25-MAR-2003 to correct PN field.)
XX
XX
SQ Sequence 43 AA;
Query Match 77.8%; Score 84; DB 16; Length 43;
Best Local Similarity 76.5%; Pred. No. 0.00016;
Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
QY 1 DCPSEWSSYEGFCYKPF 17
Db 1 DCPSDWSSHEGHCYKVF 17
RESULT 12
AAR23889
ID AAR23889 standard; Protein; 50 AA.
XX
AC AAR23889;
XX
CC 25-MAR-2003 (updated)
DT 21-NOV-1992 (first entry)
XX
XX N-terminal sequence of the earlier eluting subunit PP-beta of
DE the later eluting peak of the platelet antiadhesive peptide (PAA).
XX
XX Platelet adherence inhibitor; platelet anti-adhesive;
XX antithrombotic agent; von Willebrand Factor;
KW platelet glycoprotein GPIb-IX complex.
XX
XX Pseudocerastes persicus.
XX
XX WO9208472-A1.
XX
XX 29-MAY-1992.
XX
XX 14-NOV-1991; 91WO-US08516.
XX
PR 16-NOV-1990; 90US-0614443.
XX
XX (CORT-) COR THERAPEUTICS INC.
XX
XX Scarborough RM;
XX
XX WPI; 1992-199936/24.
XX
XX Platelet antiadhesive peptide(s) obtd. from snake venom - also
PT inhibit thrombus formation; for treatment of arteriosclerosis,
PT atherosclerosis, acute myocardial infarction, chronic unstable
PT angina, etc.
XX
XX Claim 7; Page 30; 5pp; English.
XX
XX The PAA was purified from a solution of snake venom. The earlier
CC eluting subunit, PP-beta was subjected to Edman degradation for 50
CC cycles to obtain the sequence in AAR23889. The later eluting
CC sequence - the PP-alpha chain was determined for 31 cycles to give
CC the SQ in AAR23890.
CC (Updated on 25-MAR-2003 to correct PN field.)
XX

SQ Sequence 50 AA;
Query Match 77.8%; Score 84; DB 13; Length 50;
Best Local Similarity 76.5%; Pred. No. 0.00019;
Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
QY 1 DCPSEWSSYEGFCYKPF 17
Db 1 DCPSDWSSHEGHCYKVF 17
RESULT 13
AAR72233
ID AAR72233 standard; peptide; 52 AA.
XX
AC AAR72233;
XX
DT 25-MAR-2003 (updated)
DT 04-DEC-1995 (first entry)
XX
XX Vipera palestinae venom derived peptide N-terminal fragment.
DE Vipera palestinae; venom; N-terminal fragment; antithrombotic agent;
KW platelet binding; von Willebrand factor.
XX
OS Vipera palestinae.
XX
XX WO9509183-A1.
XX
XX 06-APR-1995.
XX
XX 27-SEP-1994; 94WO-JP01583.
XX
PR 28-SEP-1993; 93JP-0241666.
PR 14-JAN-1994; 94JP-0002691.
PR 10-JUN-1994; 94JP-0128518.
XX
XX (AJIN) AJINOMOTO KK.
XX
XX Fukuchi N, Ishii K, Kaide K, Kobayashi T;
XX WPI; 1995-147392/19.
XX
XX Peptide derived from Vipera palestinae venom - inhibits binding
PT of platelets to von Willebrand factor, useful as antithrombotic
PT agent
XX
XX Claim 4; Page 18; 37pp; Japanese.
XX
CC AAR72233 is a Vipera palestinae venom derived N-terminal fragment,
CC the full peptide is given in AAR72235. A peptide compsn. comprising
CC AAR72235 and AAR72236 is claimed, it inhibits the binding of platelets
CC to von Willebrand factors and can therefore be used as an anti-
CC thrombotic agent.
CC (Updated on 25-MAR-2003 to correct PN field.)
XX
XX
SQ Sequence 52 AA;
Query Match 77.8%; Score 84; DB 16; Length 52;
Best Local Similarity 76.5%; Pred. No. 0.00019;
Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
QY 1 DCPSEWSSYEGFCYKPF 17
Db 3 DCPSDWSSHEGHCYKVF 19
RESULT 14
AAR72236
ID AAR72236 standard; peptide; 127 AA.
XX
XX AAR72236;
XX

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DT 25-MAR-2003 (updated)
DT 04-DEC-1995 (first entry)
DE Vipera palestinae venom derived peptide.
XX
XX Vipera palestinae; venom; antithrombotic agent;
KW platelet binding; von Willebrand factor.
XX
OS Vipera palestinae.
XX
XX WO9509183-A1.
XX
XX 06-APR-1995.
XX
XX 27-SEP-1994; 94WO-JP01583.
XX
XX 28-SEP-1993; 93JP-0241666.
PR 14-JAN-1994; 94JP-0002691.
PR 10-JUN-1994; 94JP-0128518.
XX
XX (AJIN ) AJINOMOTO KK.
XX
XX Fukuchi N, Ishii K, Kaida K, Kobayashi T;
XX WPI; 1995-147392/19.
XX
XX Peptide derived from Vipera palestinae venom - inhibits binding
XX of platelets to von Willebrand factor, useful as antithrombotic
XX agent
XX
XX Claim 5; Pages 19-20; 37pp; Japanese.
XX
XX AAR72235 is a Vipera palestinae venom derived peptide. A peptide
XX compen. comprising AAR72235 and AAR72236 is claimed, it inhibits the
XX binding of platelets to von Willebrand factors and can therefore
XX be used as an anti- thrombotic agent.
XX (Updated on 25-MAR-2003 to correct PN field.)
XX
XX SQ Sequence 127 AA;
XX
XX Query Match 77.8%; Score 84; DB 16; Length 127;
XX Best Local Similarity 76.5%; Pred. No. 0.00043;
XX Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 DCPSEWSSYEGFCYKPF 17
Db ||||:||||:||||
1 DCPSDWSHSHGHCYKVF 17

RESULT 15
AAR72235
ID AAR72235 standard; peptide; 132 AA.
XX
XX AC AAR72235;
XX
XX 25-MAR-2003 (updated)
DT 04-DEC-1995 (first entry)
XX
DE Vipera palestinae venom derived peptide.
XX
XX Vipera palestinae; venom; antithrombotic agent;
KW platelet binding; von Willebrand factor.
XX
XX Vipera palestinae.
XX
XX WO9509183-A1.
XX
XX 06-APR-1995.
XX
XX 27-SEP-1994; 94WO-JP01583.
XX
XX 28-SEP-1993; 93JP-0241666.
PR 14-JAN-1994; 94JP-0002691.
PR 10-JUN-1994; 94JP-0128518.
XX
XX (AJIN ) AJINOMOTO KK.
XX
XX Fukuchi N, Ishii K, Kaida K, Kobayashi T;
XX WPI; 1995-147392/19.
XX
XX Peptide derived from Vipera palestinae venom - inhibits binding
XX of platelets to von Willebrand factor, useful as antithrombotic
XX agent
XX
XX Claim 5; Pages 19-20; 37pp; Japanese.
XX
XX AAR72235 is a Vipera palestinae venom derived peptide. A peptide
XX compen. comprising AAR72235 and AAR72236 is claimed, it inhibits the
XX binding of platelets to von Willebrand factors and can therefore
XX be used as an anti- thrombotic agent.
XX (Updated on 25-MAR-2003 to correct PN field.)
XX
XX SQ Sequence 132 AA;
XX
XX Query Match 77.8%; Score 84; DB 16; Length 132;
XX Best Local Similarity 76.5%; Pred. No. 0.00044;
XX Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 DCPSEWSSYEGFCYKPF 17
Db ||||:||||:||||
3 DCPSDWSHSHGHCYKVF 19

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PR 10-JUN-1994; 94JP-0128518.
XX
XX (AJIN ) AJINOMOTO KK.
XX
XX Fukuchi N, Ishii K, Kaida K, Kobayashi T;
XX WPI; 1995-147392/19.
XX
XX Peptide derived from Vipera palestinae venom - inhibits binding
XX of platelets to von Willebrand factor, useful as antithrombotic
XX agent
XX
XX Claim 5; Page 19; 37pp; Japanese.
XX
XX AAR72235 is a Vipera palestinae venom derived peptide. A peptide
XX compen. comprising AAR72235 and AAR72236 is claimed, it inhibits the
XX binding of platelets to von Willebrand factors and can therefore
XX be used as an anti- thrombotic agent.
XX (Updated on 25-MAR-2003 to correct PN field.)
XX
XX SQ Sequence 132 AA;
XX
XX Query Match 77.8%; Score 84; DB 16; Length 132;
XX Best Local Similarity 76.5%; Pred. No. 0.00044;
XX Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 DCPSEWSSYEGFCYKPF 17
Db ||||:||||:||||
3 DCPSDWSHSHGHCYKVF 19

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OM protein - protein search, using sw model

Run on: December 8, 2003, 09:50:40 ; Search time 3.69143 Seconds
(without alignments)
194.853 Million cell updates/sec

Title: US-09-938-114-4

Perfect score: 108

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Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Issued Patents AA:*

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6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	86	79.6	21	2	US-08-612-840A-3
3	86	79.6	117	1	US-07-614-443A-2
4	86	79.6	117	1	US-08-294-859-2
5	86	79.6	117	1	US-08-481-676-2
6	86	79.6	123	1	US-07-893-929A-4
7	86	79.6	123	5	PCT-US92-10344-4
8	84	77.8	50	1	US-07-614-443A-5
9	84	77.8	50	1	US-08-294-859-5
10	84	77.8	50	1	US-08-481-676-5
11	83	76.9	38	2	US-08-612-840A-1
12	83	76.9	126	2	US-08-612-840A-2
13	83	76.9	127	1	US-07-614-443A-1
14	83	76.9	127	1	US-08-294-859-1
15	83	76.9	127	1	US-08-481-676-1
16	83	76.9	149	2	US-08-612-840A-8
17	81	75.0	29	4	US-09-058-740-3
18	81	75.0	129	4	US-09-058-740-2
19	80	74.1	107	1	US-07-893-929A-6
20	80	74.1	107	5	PCT-US92-10344-6
21	80	74.1	128	1	US-07-893-929A-8
22	80	74.1	128	5	PCT-US92-10344-8
23	79	73.1	131	1	US-07-893-929A-1
24	79	73.1	131	5	PCT-US92-10344-1
25	74	68.5	125	1	US-07-893-929A-3
26	74	68.5	125	5	PCT-US92-10344-3
27	69	63.9	130	1	US-07-893-929A-7

28	69	63.9	130	5	PCT-US92-10344-7	Sequence 7, Appli
29	69	63.9	132	1	US-07-893-929A-5	Sequence 5, Appli
30	69	63.9	132	5	PCT-US92-10344-5	Sequence 5, Appli
31	68	63.0	15	1	US-08-551-128A-1	Sequence 1, Appli
32	67	62.0	123	1	US-07-893-929A-10	Sequence 10, Appli
33	67	62.0	123	5	PCT-US92-10344-10	Sequence 10, Appli
34	65	60.2	30	2	US-08-894-403-3	Sequence 3, Appli
35	64	59.3	22	1	US-07-614-443A-7	Sequence 7, Appli
36	64	59.3	22	1	US-08-294-859-7	Sequence 7, Appli
37	64	59.3	22	1	US-08-481-676-7	Sequence 7, Appli
38	64	59.3	133	1	US-07-893-929A-9	Sequence 9, Appli
39	64	59.3	133	5	PCT-US92-10344-9	Sequence 9, Appli
40	61	56.5	15	1	US-08-551-128A-2	Sequence 2, Appli
41	60	55.6	20	1	US-07-614-443A-4	Sequence 4, Appli
42	60	55.6	20	1	US-08-294-859-4	Sequence 4, Appli
43	60	55.6	20	1	US-08-481-676-4	Sequence 4, Appli
44	60	55.6	30	2	US-08-894-403-4	Sequence 4, Appli
45	59	54.6	31	1	US-07-614-443A-6	Sequence 6, Appli

ALIGNMENTS

RESULT 1

US-09-058-740-4

; Sequence 4, Application US/09058740

; Patent No. 6489451

; GENERAL INFORMATION:

APPLICANT: Chun Wang, Benjamin XY Li, Xin Cheng,

Jing Liu, Li-Wen Niu, Wan-Zhi Huang,

Zhen-Yu Xu, Dan Luo, Lian-Di Kang,

Jin-Guo Ding, Fang Rong, Yan Liu and

Hui-Ran Chen

TITLE OF INVENTION: AN ANTITHROMBOSIS ENZYME FROM THE SNAKE

VENOM OF AGKISTRODON ACUTUS

NUMBER OF SEQUENCES: 12

CORRESPONDENCE ADDRESS:

ADDRESSEE: Lyon & Lyon

STREET: 633 West Fifth Street

Suite 4700

CITY: Los Angeles

STATE: California

COUNTRY: U.S.A.

ZIP: 90071-2066

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

COMPUTER: IBM Compatible

OPERATING SYSTEM: IBM P.C. DOS 5.0

SOFTWARE: FastSeq for Windows 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/058,740

FILING DATE: 10-Apr-1998

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: <Unknown>

FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Chen, Anthony C.

REGISTRATION NUMBER: 38,673

REFERENCE/DOCKET NUMBER: 233/298

TELECOMMUNICATION INFORMATION:

TELEPHONE: (213) 489-1600

TELEFAX: (213) 955-0440

TELEX: 67-3510

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 17 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: Peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 4:

US-09-058-740-4

Query Match 100.0%; Score 108; DB 4; Length 17;
Best Local Similarity 100.0%; Pred. No. 3.8e-09;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DCPSEWSSYEGFCYKPF 17
| | | | | | | | | | | | | | | | |
Db 1 DCPSEWSSYEGFCYKPF 17

RESULT 2

US-08-612-840A-3
; Sequence 3, Application US/08612840A
; Patent No. 5856126

GENERAL INFORMATION:

APPLICANT: FUKUCHI, Naoyuki
APPLICANT: YAMAMOTO, Hiroshi
APPLICANT: NAGANO, Mitsuyo
APPLICANT: KITO, Morikazu
APPLICANT: TANAKA, Akiko
APPLICANT: ISHII, Koichi
APPLICANT: KOBAYASHI, Tsuyoshi
APPLICANT: YOSHIMOTO, Ryota
TITLE OF INVENTION: PEPTIDE HAVING ANTI-THROMBUS ACTIVITY AND
METHOD OF PRODUCING THE SAME
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Obion, Spivak, McClelland, Maier & Neustadt, P.C.
STREET: 1755 S. Jefferson Davis Highway, Suite 400
CITY: Arlington
STATE: VA
COUNTRY: USA
ZIP: 22202

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/612.840A
FILING DATE: 20-MAR-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 5-236975
FILING DATE: 22-SEP-1993

ATTORNEY/AGENT INFORMATION:

NAME: No. 5856126man F. Oblon
REGISTRATION NUMBER: 24.618
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-3000
TELEFAX: 703-413-2220
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-612-840A-3

Query Match 79.6%; Score 86; DB 2; Length 21;
Best Local Similarity 76.5%; Pred. No. 6e-05;
Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 DCPSEWSSYEGFCYKPF 17
| | | | | | | | | | | | | | | | |
Db 1 DCPSEWSSYEGFCYKPF 17

RESULT 3

US-07-614-443A-2
; Sequence 2, Application US/07614443A
; Patent No. 5342830

GENERAL INFORMATION:

APPLICANT: SCARBOROUGH, ROBERT M.
TITLE OF INVENTION: ANTI-THROMBOSIS AGENTS
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morrison & Foerster
STREET: 755 Page Mill Road
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/614.443A
FILING DATE: 19901116
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Murashige, Kate H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 22803-20003.00
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 813-5600
TELEFAX: (415) 494-0792
TELEX: 706141
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 117 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-07-614-443A-2

Query Match 79.6%; Score 86; DB 1; Length 117;
Best Local Similarity 76.5%; Pred. No. 3.5e-05;
Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 DCPSEWSSYEGFCYKPF 17
| | | | | | | | | | | | | | | | |
Db 1 DCPSEWSSYEGFCYKPF 17

RESULT 4

US-08-294-859-2
; Sequence 2, Application US/08294859
; Patent No. 5679542

GENERAL INFORMATION:

APPLICANT: SCARBOROUGH, ROBERT M.
TITLE OF INVENTION: ANTI-THROMBOSIS AGENTS
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morrison & Foerster
STREET: 2000 Pennsylvania Ave. N.W., Suite 5500
CITY: Washington, D.C.
COUNTRY: USA
ZIP: 20006-1888

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/294.859
FILING DATE: 29-AUG-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Murashige, Kate H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 2803-0003.10
TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 887-1500
 TELEFAX: (202) 887-0763
 TELEX: 90-4030
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 117 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 US-08-294-859-2

Query Match 79.6%; Score 86; DB 1; Length 117;
 Best Local Similarity 76.5%; Pred. No. 3.5e-05;
 Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 DCPSEWSSYEGFCYKPF 17
 Db 1 DCPDWSYEGHCYRVF 17

RESULT 5

US-08-481-676-2
 Sequence 2, Application US/08481676
 Patent No. 5744584
 GENERAL INFORMATION:
 APPLICANT: SCARBOROUGH, ROBERT M.
 TITLE OF INVENTION: ANTITHROMBOSIS AGENTS
 NUMBER OF SEQUENCES: 7
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Morrison & Foerster
 STREET: 2000 Pennsylvania Ave. N.W., Suite 5500
 CITY: Washington, D.C.
 COUNTRY: USA
 ZIP: 20006-1888

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/481,676
 FILING DATE: 07-JUN-1995
 CLASSIFICATION: 514
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/294,859
 FILING DATE: 29-AUG-1994
 ATTORNEY/AGENT INFORMATION:
 NAME: Murashige, Kate H.
 REGISTRATION NUMBER: 29,959
 REFERENCE/DOCKET NUMBER: 2803-0003.10
 TELEPHONE: (202) 887-1500
 TELEFAX: (202) 887-0763
 TELEX: 90-4030

INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 117 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 US-08-481-676-2

Query Match 79.6%; Score 86; DB 1; Length 117;
 Best Local Similarity 76.5%; Pred. No. 3.5e-05;
 Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 DCPSEWSSYEGFCYKPF 17
 Db 1 DCPDWSYEGHCYRVF 17

RESULT 6

US-07-893-929A-4

Sequence 4, Application US/07893929A
 Patent No. 5336667
 GENERAL INFORMATION:
 APPLICANT: Kirby, Edward P.
 APPLICANT: Peng, Man-ling
 TITLE OF INVENTION: Alboaggregins: Platelet
 TITLE OF INVENTION: Agonists Which Bind To Platelet
 NUMBER OF SEQUENCES: 10
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Temple University - Of The Common-
 ADDRESSEE: wealth System of Higher Education
 STREET: 406 University Services Building
 CITY: Philadelphia
 STATE: Pennsylvania
 COUNTRY: U.S.A.
 ZIP: 19122

COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette, 3.50 inch, 720 Kb

COMPUTER: IBM PS/2
 OPERATING SYSTEM: MS-DOS
 SOFTWARE: WordPerfect 5.1
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/07/893,929A
 FILING DATE: 19920605

CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/803,630
 FILING DATE: December 3, 1991
 ATTORNEY/AGENT INFORMATION:
 NAME: Monaco, Daniel A.
 REGISTRATION NUMBER: 30,480
 REFERENCE/DOCKET NUMBER: 6056-126 (CIP) 1
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (215) 568-8383
 TELEFAX: (215) 568-5549
 TELEX: No. 5336667e
 INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 123 amino acids
 TYPE: AMINO ACID
 TOPOLOGY: linear
 US-07-893-929A-4

Query Match 79.6%; Score 86; DB 1; Length 123;
 Best Local Similarity 76.5%; Pred. No. 3.6e-05;
 Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 DCPSEWSSYEGFCYKPF 17
 Db 1 DCPDWSYEGHCYRVF 17

RESULT 7

PCT-US92-10344-4
 Sequence 4, Application PC/TUS9210344
 GENERAL INFORMATION:

APPLICANT: Kirby, Edward P.
 APPLICANT: Peng, Man-ling
 TITLE OF INVENTION: Alboaggregins: Platelet
 TITLE OF INVENTION: Agonists Which Bind To Platelet
 NUMBER OF SEQUENCES: 10
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Temple University - Of The Common-
 ADDRESSEE: wealth System of Higher Education
 STREET: 406 University Services Building
 CITY: Philadelphia
 STATE: Pennsylvania
 COUNTRY: U.S.A.
 ZIP: 19122

COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette, 3.50 inch, 720 Kb

COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/10344
FILING DATE: 19921201
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/803,630
FILING DATE: December 3, 1991
ATTORNEY/AGENT INFORMATION:
NAME: Monaco, Daniel A.
REGISTRATION NUMBER: 30,480
REFERENCE/DOCKET NUMBER: 6056-126 (CIP) 1
TELEPHONE: (215) 568-8383
TELEFAX: (215) 568-5549
TELEX: None
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 123 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
PCT-US92-10344-4

Query Match 79.6%; Score 86; DB 5; Length 123;
Best Local Similarity 76.5%; Pred. No. 3.6e-05;
Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 DCPSEWSSYEGFCYKPF 17
Db 1 DCPSDWSSYEGHCYRVF 17

RESULT 8
US-07-614-443A-5
Sequence 5, Application US/07614443A
Patent No. 5342830
GENERAL INFORMATION:
APPLICANT: SCARBOROUGH, ROBERT M.
TITLE OF INVENTION: ANTITHROMBOSIS AGENTS
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morrison & Foerster
STREET: 755 Page Mill Road
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/614,443A
FILING DATE: 19901116
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Murashige, Kate H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 22803-20003.00
TELEPHONE: (415) 813-5600
TELEFAX: (415) 494-0792
TELEX: 706141
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 50 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-07-614-443A-5

Query Match 77.8%; Score 84; DB 1; Length 50;
Best Local Similarity 76.5%; Pred. No. 2.8e-05;
Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 DCPSEWSSYEGFCYKPF 17
Db 1 DCPSDWSSYEGHCYKVF 17

RESULT 9
US-08-294-859-5
Sequence 5, Application US/08294859
Patent No. 5679542
GENERAL INFORMATION:
APPLICANT: SCARBOROUGH, ROBERT M.
TITLE OF INVENTION: ANTITHROMBOSIS AGENTS
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morrison & Foerster
STREET: 2000 Pennsylvania Ave. N.W., Suite 5500
CITY: Washington, D.C.
COUNTRY: USA
ZIP: 20006-1888
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/294,859
FILING DATE: 29-AUG-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Murashige, Kate H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 2803-0003.10
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
TELEFAX: (202) 887-0763
TELEX: 90-4030
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 50 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-294-859-5

Query Match 77.8%; Score 84; DB 1; Length 50;
Best Local Similarity 76.5%; Pred. No. 2.8e-05;
Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 DCPSEWSSYEGFCYKPF 17
Db 1 DCPSDWSSYEGHCYKVF 17

RESULT 10
US-08-481-676-5
Sequence 5, Application US/08481676
Patent No. 5744584
GENERAL INFORMATION:
APPLICANT: SCARBOROUGH, ROBERT M.
TITLE OF INVENTION: ANTITHROMBOSIS AGENTS
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morrison & Foerster
STREET: 2000 Pennsylvania Ave. N.W., Suite 5500
CITY: Washington, D.C.
COUNTRY: USA
ZIP: 20006-1888
COMPUTER READABLE FORM:

;/ MEDIUM TYPE: Floppy disk
;/ COMPUTER: IBM PC compatible
;/ OPERATING SYSTEM: PC-DOS/MS-DOS
;/ SOFTWARE: PatentIn Release #1.0, Version #1.25
;/ CURRENT APPLICATION DATA:
;/ APPLICATION NUMBER: US/08/481,676
;/ FILING DATE: 07-JUN-1995
;/ CLASSIFICATION: 514
;/ PRIOR APPLICATION DATA:
;/ APPLICATION NUMBER: US 08/294,859
;/ FILING DATE: 29-AUG-1994
;/ ATTORNEY/AGENT INFORMATION:
;/ NAME: Murashige, Kate H.
;/ REGISTRATION NUMBER: 29,959
;/ REFERENCE/DOCKET NUMBER: 2803-0003.10
;/ TELECOMMUNICATION INFORMATION:
;/ TELEPHONE: (202) 887-1500
;/ TELEFAX: (202) 887-0763
;/ TELEX: 90-4030
;/ INFORMATION FOR SEQ ID NO: 5:
;/ LENGTH: 50 amino acids
;/ TYPE: amino acid
;/ STRANDEDNESS: single
;/ TOPOLOGY: linear
;/ US-08-481-676-5

Query Match 77.8%; Score 84; DB 1; Length 50;
Best Local Similarity 76.5%; Pred. No. 2.8e-05;
Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 DCPSEWSYEGFCYKPF 17
Db 1 DCPSDWSHGHGCHYKPF 17
|||||:|||||

RESULT 11
US-08-612-840A-1
; Sequence 1, Application US/08612840A
; Patent No. 5856126
; GENERAL INFORMATION:
; APPLICANT: FUKUCHI, Naoyuki
; APPLICANT: YAMAMOTO, Hiroshi
; APPLICANT: NAGANO, Mitsuyo
; APPLICANT: KITO, Morikazu
; APPLICANT: TANAKA, Akiko
; APPLICANT: ISHII, Koichi
; APPLICANT: KOBAYASHI, Tsuyoshi
; APPLICANT: YOSHIMOTO, Ryota
; TITLE OF INVENTION: PEPTIDE HAVING ANTI-THROMBUS ACTIVITY AND
; TITLE OF INVENTION: METHOD OF PRODUCING THE SAME
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Oblon, Spivak, McClelland, Maier & Neustadt, P.C.
; STREET: 1755 S. Jefferson Davis Highway, Suite 400
; CITY: Arlington
; STATE: VA
; COUNTRY: USA
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/612,840A
; FILING DATE: 20-MAR-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 5-236975
; FILING DATE: 22-SEP-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5856126man F. Oblon

;/ REGISTRATION NUMBER: 24,618
;/ TELECOMMUNICATION INFORMATION:
;/ TELEPHONE: 703-413-3000
;/ TELEFAX: 703-413-2220
;/ INFORMATION FOR SEQ ID NO: 1:
;/ SEQUENCE CHARACTERISTICS:
;/ LENGTH: 38 amino acids
;/ TYPE: amino acid
;/ TOPOLOGY: linear
;/ MOLECULE TYPE: peptide
;/ US-08-612-840A-1

Query Match 76.9%; Score 83; DB 2; Length 38;
Best Local Similarity 70.6%; Pred. No. 2.9e-05;
Matches 12; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 DCPSEWSYEGFCYKPF 17
Db 3 ECPGSSYDRYKPF 19
|||||:|||||

RESULT 12
US-08-612-840A-2
; Sequence 2, Application US/08612840A
; Patent No. 5856126
; GENERAL INFORMATION:
; APPLICANT: FUKUCHI, Naoyuki
; APPLICANT: YAMAMOTO, Hiroshi
; APPLICANT: NAGANO, Mitsuyo
; APPLICANT: KITO, Morikazu
; APPLICANT: TANAKA, Akiko
; APPLICANT: ISHII, Koichi
; APPLICANT: KOBAYASHI, Tsuyoshi
; APPLICANT: YOSHIMOTO, Ryota
; TITLE OF INVENTION: PEPTIDE HAVING ANTI-THROMBUS ACTIVITY AND
; TITLE OF INVENTION: METHOD OF PRODUCING THE SAME
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Oblon, Spivak, McClelland, Maier & Neustadt, P.C.
; STREET: 1755 S. Jefferson Davis Highway, Suite 400
; CITY: Arlington
; STATE: VA
; COUNTRY: USA
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/612,840A
; FILING DATE: 20-MAR-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 5-236975
; FILING DATE: 22-SEP-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5856126man F. Oblon
;/ TELECOMMUNICATION INFORMATION:
;/ TELEPHONE: 703-413-3000
;/ TELEFAX: 703-413-2220
;/ INFORMATION FOR SEQ ID NO: 2:
;/ SEQUENCE CHARACTERISTICS:
;/ LENGTH: 126 amino acids
;/ TYPE: amino acid
;/ TOPOLOGY: linear
;/ MOLECULE TYPE: peptide
;/ US-08-612-840A-2

Query Match 76.9%; Score 83; DB 2; Length 126;
Best Local Similarity 70.6%; Pred. No. 9.9e-05;
Matches 12; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1 DCPSEWSSYEGFCYKPF 17
:|||||: :|||||
Db 3 ECPSGWSSYDRYCYKPF 19

RESULT 13

US-07-614-443A-1
; Sequence 1, Application US/07614443A
; Patent No. 5342830
; GENERAL INFORMATION:
; APPLICANT: SCARBOROUGH, ROBERT M.
; TITLE OF INVENTION: ANTI-THROMBOSIS AGENTS
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morrison & Foerster
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/614,443A
; FILING DATE: 19901116
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Murashige, Kate H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 22803-20003.00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 127 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-07-614-443A-1

Query Match 76.9%; Score 83; DB 1; Length 127;
Best Local Similarity 70.6%; Pred. No. 0.0001;
Matches 12; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1 DCPSEWSSYEGFCYKPF 17
:|||||: :|||||
Db 3 ECPSGWSSYDRYCYKPF 19

RESULT 14

US-08-294-859-1
; Sequence 1, Application US/08294859
; Patent No. 5679542
; GENERAL INFORMATION:
; APPLICANT: SCARBOROUGH, ROBERT M.
; TITLE OF INVENTION: ANTI-THROMBOSIS AGENTS
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morrison & Foerster
; STREET: 2000 Pennsylvania Ave. N.W., Suite 5500
; CITY: Washington, D.C.
; COUNTRY: USA
; ZIP: 20006-1888
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/294,859
; FILING DATE: 29-AUG-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Murashige, Kate H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 2803-0003.10
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 887-1500
; TELEFAX: (202) 887-0763
; TELEX: 90-4030
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 127 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-294-859-1

Query Match 76.9%; Score 83; DB 1; Length 127;
Best Local Similarity 70.6%; Pred. No. 0.0001;
Matches 12; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1 DCPSEWSSYEGFCYKPF 17
:|||||: :|||||
Db 3 ECPSGWSSYDRYCYKPF 19

RESULT 15

US-08-481-676-1
; Sequence 1, Application US/08481676
; Patent No. 5744584
; GENERAL INFORMATION:
; APPLICANT: SCARBOROUGH, ROBERT M.
; TITLE OF INVENTION: ANTI-THROMBOSIS AGENTS
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morrison & Foerster
; STREET: 2000 Pennsylvania Ave. N.W., Suite 5500
; CITY: Washington, D.C.
; COUNTRY: USA
; ZIP: 20006-1888
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/481,676
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/294,859
; FILING DATE: 29-AUG-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Murashige, Kate H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 2803-0003.10
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 887-1500
; TELEFAX: (202) 887-0763
; TELEX: 90-4030
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 127 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-481-676-1

Query Match 76.9%; Score 83; DB 1; Length 127;

Best Local Similarity 70.6%; Pred. No. 0.0001;
Matches 12; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1 DCPSEWSSYEGFCYKPF 17
Db 3 ECPGWSYDRYCYKPF 19

Search completed: December 8, 2003, 09:56:26
Job time : 4.69143 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 8, 2003, 09:54:55 ; Search time 6.99429 Seconds
(without alignments)
452.044 Million cell updates/sec

Title: US-09-938-114-4

Perfect score: 108

Sequence: 1 DCPSEWSYRGFCYKPF 17

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 684280 seqs, 185983659 residues

Total number of hits satisfying chosen parameters: 684280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA:*

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12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
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16: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	ID	Description
1	108	100.0	17	11	US-09-938-114-4
2	83	76.9	149	10	US-09-969-763-3
3	81	75.0	29	11	US-09-938-114-3
4	81	75.0	110	10	US-09-969-763-10
5	81	75.0	129	11	US-09-938-114-2
6	78	72.2	151	10	US-09-929-230-2
7	78	72.2	151	12	US-10-226-420-2
8	74	68.5	126	10	US-09-969-763-1
9	71	65.7	152	10	US-09-929-230-5
10	71	65.7	152	12	US-10-226-420-5
11	66	61.1	144	10	US-09-929-230-8
12	66	61.1	144	12	US-10-226-420-8
13	61	56.5	1456	10	US-09-870-759-95
14	61	56.5	1456	12	US-09-751-708A-95
15	58	53.7	119	9	US-09-764-870-302
					Sequence 4, Appli
					Sequence 3, Appli
					Sequence 10, Appli
					Sequence 2, Appli
					Sequence 1, Appli
					Sequence 5, Appli
					Sequence 8, Appli
					Sequence 95, Appli
					Sequence 95, Appli
					Sequence 302, Appli

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58 53.7 119 15 US-10-125-540-302 Sequence 302, App
58 53.7 293 10 US-09-978-295A-231 Sequence 231, App
58 53.7 293 10 US-09-978-697-231 Sequence 231, App
58 53.7 293 10 US-09-978-192A-231 Sequence 231, App
58 53.7 293 10 US-09-999-832A-231 Sequence 231, App
58 53.7 293 11 US-09-978-189-231 Sequence 231, App
58 53.7 293 11 US-09-978-608A-231 Sequence 231, App
58 53.7 293 11 US-09-978-585A-231 Sequence 231, App
58 53.7 293 11 US-09-978-191A-231 Sequence 231, App
58 53.7 293 11 US-09-978-403A-231 Sequence 231, App
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58 53.7 293 11 US-09-999-833A-231 Sequence 231, App
58 53.7 293 11 US-09-981-915A-231 Sequence 231, App
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58 53.7 293 11 US-09-999-830A-231 Sequence 231, App
58 53.7 293 11 US-09-978-757A-231 Sequence 231, App
58 53.7 293 11 US-09-978-187B-231 Sequence 231, App
58 53.7 293 11 US-09-978-643A-231 Sequence 231, App
58 53.7 293 12 US-09-978-375A-231 Sequence 231, App
58 53.7 293 12 US-09-978-188A-231 Sequence 231, App
58 53.7 293 12 US-09-978-298A-231 Sequence 231, App
58 53.7 293 12 US-10-137-870-422 Sequence 422, App
58 53.7 293 12 US-10-140-018-422 Sequence 422, App
58 53.7 293 12 US-10-140-021-422 Sequence 422, App
58 53.7 293 12 US-10-140-274-422 Sequence 422, App
58 53.7 293 12 US-10-140-471-422 Sequence 422, App
58 53.7 293 12 US-10-140-807-422 Sequence 422, App

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ALIGNMENTS

RESULT 1

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US-09-938-114-4
; Sequence 4, Application US/09938114
; Publication No. US20030022350A1
; GENERAL INFORMATION:
; APPLICANT: Chun Wang, Benjamin XY Li, Xin Cheng,
; Jing Liu, Li-Wen Niu, Wan-Zhi Huang,
; Zhen-yu Xu, Dan Luo, Lian-Di Kang,
; Jin-Guo Ding, Fang Rong, Yan Liu and
; Hui-Ran Chen
; TITLE OF INVENTION: AN ANTITHROMBOSIS ENZYME FROM THE SNAKE
; VENOM OF AGKISTRODON ACUTUS
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FASTSEQ for Windows 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/938,114
; FILING DATE: 23-Aug-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/058,740
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Chen, Anthony C.
; REGISTRATION NUMBER: 38,673
; REFERENCE/DOCKET NUMBER: 233/298

```

```
;
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-938-114-4
Query Match 100.0%; Score 108; DB 11; Length 17;
Best Local Similarity 100.0%; Pred. No. 8.9e-09;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DCPSEWSSYEGFCYKPF 17
Db 1 DCPSEWSSYEGFCYKPF 17

RESULT 2
US-09-969-763-3
; Sequence 3, Application US/09969763
; Publication No. US20020198363A1
; GENERAL INFORMATION:
; APPLICANT: FUKUCHI, NAOYUKI
; APPLICANT: KITO, MORIKAZU
; APPLICANT: KAWAHARA, TAKASHI
; APPLICANT: FUTAKI, FUMIE
; APPLICANT: ISHIKAWA, KOHJI
; APPLICANT: SUZUKI, EIICHIRO
; APPLICANT: GONDOH, KEIKO
; APPLICANT: SHIMBA, NOBUHISA
; APPLICANT: YAMADA, NAOYUKI
; TITLE OF INVENTION: PROTEIN HAVING ANTITHROMBOTIC ACTIVITY AND METHOD FOR PRODUCING IT
; FILE REFERENCE: 214760US0
; CURRENT APPLICATION NUMBER: US/09/969,763
; CURRENT FILING DATE: 2000-10-25
; PRIOR APPLICATION NUMBER: JP 2000-305279
; PRIOR FILING DATE: 2000-10-04
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 3
; LENGTH: 149
; TYPE: PRT
; ORGANISM: Crocalus harridus
US-09-969-763-3

Query Match 76.9%; Score 83; DB 10; Length 149;
Best Local Similarity 70.6%; Pred. No. 0.00024;
Matches 12; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 DCPSEWSSYEGFCYKPF 17
Db 26 ECPGSSSYDRYCYKPF 42

RESULT 3
US-09-938-114-3
; Sequence 3, Application US/09938114
; Publication No. US20030022350A1
; GENERAL INFORMATION:
; APPLICANT: Chun Wang, Benjamin XY Li, Xin Cheng,
; Jing Liu, Li-Wen Niu, Wan-Zhi Huang,
; Zhen-Yu Xu, Dan Luo, Lian-Di Kang,
; Jin-Guo Ding, Fang Rong, Yan Liu and
; Hui-Ran Chen
; TITLE OF INVENTION: AN ANTITHROMBOTIC ENZYME FROM THE SNAKE
; VENOM OF AGKISTRODON ACUTUS
; NUMBER OF SEQUENCES: 12
```

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;
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: PastSeq for Windows 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/938,114
; FILING DATE: 23-Aug-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/058,740
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Chen, Anthony C.
; REGISTRATION NUMBER: 38,673
; REFERENCE/DOCKET NUMBER: 233/298
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 29 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-938-114-3

Query Match 75.0%; Score 81; DB 11; Length 29;
Best Local Similarity 76.5%; Pred. No. 9.9e-05;
Matches 13; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 DCPSEWSSYEGFCYKPF 17
Db 1 DCPSEWSSYEGHCYKVF 17

RESULT 4
US-09-969-763-10
; Sequence 10, Application US/09969763
; Publication No. US20020198363A1
; GENERAL INFORMATION:
; APPLICANT: FUKUCHI, NAOYUKI
; APPLICANT: KITO, MORIKAZU
; APPLICANT: KAWAHARA, TAKASHI
; APPLICANT: FUTAKI, FUMIE
; APPLICANT: ISHIKAWA, KOHJI
; APPLICANT: SUZUKI, EIICHIRO
; APPLICANT: GONDOH, KEIKO
; APPLICANT: SHIMBA, NOBUHISA
; APPLICANT: YAMADA, NAOYUKI
; TITLE OF INVENTION: PROTEIN HAVING ANTITHROMBOTIC ACTIVITY AND METHOD FOR PRODUCING IT
; FILE REFERENCE: 214760US0
; CURRENT APPLICATION NUMBER: US/09/969,763
; CURRENT FILING DATE: 2000-10-25
; PRIOR APPLICATION NUMBER: JP 2000-305279
; PRIOR FILING DATE: 2000-10-04
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 10
; LENGTH: 110
; TYPE: PRT
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; ORGANISM: ARTIFICIAL SEQUENCE
; FEATURE:
; OTHER INFORMATION: SYNTHETIC PEPTIDE
US-09-969-763-10

Query Match      75.0%; Score 81; DB 10; Length 110;
Best Local Similarity 70.6%; Pred. No. 0.00034;
Matches 12; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 DCPSEWSSYEGFCYKPF 17
Db 3 ECPGWSYRYCYKPF 19

RESULT 5
US-09-938-114-2
; Sequence 2, Application US/09938114
; Publication No. US20030022350A1
; GENERAL INFORMATION:
; APPLICANT: Chun Wang, Benjamin XY Li, Xin Cheng,
; Jing Liu, Li-Wen Niu, Wan-Zhi Huang,
; Zhen-Yu Xu, Dan Luo, Lian-Di Kang,
; Jin-Guo Ding, Fang Kong, Yan Liu and
; Hui-Ran Chen
; TITLE OF INVENTION: AN ANTITHROMBOSIS ENZYME FROM THE SNAKE
; VENOM OF AGKISTRODON ACUTUS
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSEQ for Windows 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/938,114
; FILING DATE: 23-Aug-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/058,740
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Chen, Anthony C.
; REGISTRATION NUMBER: 38,673
; REFERENCE/DOCKET NUMBER: 233/298
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 129 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-938-114-2

Query Match      75.0%; Score 81; DB 11; Length 129;
Best Local Similarity 76.5%; Pred. No. 0.0004;
Matches 13; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 DCPSEWSSYEGFCYKPF 17
Db 1 DCSWDSSYDQHCHYKVF 17
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RESULT 6
US-09-929-230-2
; Sequence 2, Application US/09929230
; Patent No. US20020161203A1
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Bishop, Paul D.
; TITLE OF INVENTION: RATTLESNAKE VENOM GLAND PROTEINS
; FILE REFERENCE: 00-72
; CURRENT APPLICATION NUMBER: US/09/929,230
; CURRENT FILING DATE: 2001-08-13
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 151
; TYPE: PRT
; ORGANISM: Sistrurus miliarius
US-09-929-230-2

Query Match      72.2%; Score 78; DB 10; Length 151;
Best Local Similarity 70.6%; Pred. No. 0.0012;
Matches 12; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 DCPSEWSSYEGFCYKPF 17
Db 20 DCPSDWSSYDQHCHYKVF 36

RESULT 7
US-10-226-420-2
; Sequence 2, Application US/10226420
; Publication No. US20030157686A1
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Bishop, Paul D.
; TITLE OF INVENTION: RATTLESNAKE VENOM GLAND PROTEINS
; FILE REFERENCE: 00-72
; CURRENT APPLICATION NUMBER: US/10/226,420
; CURRENT FILING DATE: 2002-08-21
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 151
; TYPE: PRT
; ORGANISM: Sistrurus miliarius
US-10-226-420-2

Query Match      72.2%; Score 78; DB 12; Length 151;
Best Local Similarity 70.6%; Pred. No. 0.0012;
Matches 12; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 DCPSEWSSYEGFCYKPF 17
Db 20 DCPSDWSSYDQHCHYKVF 36

RESULT 8
US-09-969-763-1
; Sequence 1, Application US/09969763
; Publication No. US20020198363A1
; GENERAL INFORMATION:
; APPLICANT: FUKUCHI, NAOYUKI
; APPLICANT: KAYAHARA, TAKASHI
; APPLICANT: FUTAKI, FUMIE
; APPLICANT: ISHIKAWA, KOHJI
; APPLICANT: SUZUKI, EIICHIRO
; APPLICANT: GONDOH, KEIKO
; APPLICANT: SHIMBA, NOBUHISA
; APPLICANT: YAMADA, NAOYUKI
; TITLE OF INVENTION: PROTEIN HAVING ANTITHROMBOTIC ACTIVITY AND METHOD FOR PRODUCING IT
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; FILE REFERENCE: 214760USO
; CURRENT APPLICATION NUMBER: US/09/969,763
; CURRENT FILING DATE: 2000-10-25
; PRIOR APPLICATION NUMBER: JP 2000-305279
; PRIOR FILING DATE: 2000-10-04
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 126
; TYPE: PRT
; ORGANISM: Crotaallus horridus
US-09-969-763-1

Query Match 68.5%; Score 74; DB 10; Length 126;
Best Local Similarity 64.7%; Pred. No. 0.0038;
Matches 11; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 1 DCPSEWSSYEGFCYKPF 17
Db 3 ECPSGWSSYDQHCYRVF 19

RESULT 9

US-09-929-230-5
; Sequence 5, Application US/09929230
; Patent No. US20020161203A1
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Bishop, Paul D.
; TITLE OF INVENTION: RATTLESNAKE VENOM GLAND PROTEINS
; FILE REFERENCE: 00-72
; CURRENT APPLICATION NUMBER: US/09/929,230
; CURRENT FILING DATE: 2001-08-13
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 152
; TYPE: PRT
; ORGANISM: Sistrurus miliarius
US-09-929-230-5

Query Match 65.7%; Score 71; DB 10; Length 152;
Best Local Similarity 64.7%; Pred. No. 0.012;
Matches 11; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 1 DCPSEWSSYEGFCYKPF 17
Db 24 DCPSGWSSYDQHCYRVF 40

RESULT 10

US-10-226-420-5
; Sequence 5, Application US/10226420
; Publication No. US20030157686A1
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Bishop, Paul D.
; TITLE OF INVENTION: RATTLESNAKE VENOM GLAND PROTEINS
; FILE REFERENCE: 00-72
; CURRENT APPLICATION NUMBER: US/10/226,420
; CURRENT FILING DATE: 2002-08-21
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 152
; TYPE: PRT
; ORGANISM: Sistrurus miliarius
US-10-226-420-5

Query Match 65.7%; Score 71; DB 12; Length 152;
Best Local Similarity 64.7%; Pred. No. 0.012;
Matches 11; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 1 DCPSEWSSYEGFCYKPF 17
Db 24 DCPSGWSSYDQHCYRVF 40

RESULT 11

US-09-929-230-8
; Sequence 8, Application US/09929230
; Patent No. US20020161203A1
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Bishop, Paul D.
; TITLE OF INVENTION: RATTLESNAKE VENOM GLAND PROTEINS
; FILE REFERENCE: 00-72
; CURRENT APPLICATION NUMBER: US/09/929,230
; CURRENT FILING DATE: 2001-08-13
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 144
; TYPE: PRT
; ORGANISM: Sistrurus miliarius
US-09-929-230-8

Query Match 61.1%; Score 66; DB 10; Length 144;
Best Local Similarity 53.3%; Pred. No. 0.059;
Matches 8; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

Qy 1 DCPSEWSSYEGFCYK 15
Db 12 DCPSDWYAYDQCYR 26

RESULT 12

US-10-226-420-8
; Sequence 8, Application US/10226420
; Publication No. US20030157686A1
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Bishop, Paul D.
; TITLE OF INVENTION: RATTLESNAKE VENOM GLAND PROTEINS
; FILE REFERENCE: 00-72
; CURRENT APPLICATION NUMBER: US/10/226,420
; CURRENT FILING DATE: 2002-08-21
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 144
; TYPE: PRT
; ORGANISM: Sistrurus miliarius
US-10-226-420-8

Query Match 61.1%; Score 66; DB 12; Length 144;
Best Local Similarity 53.3%; Pred. No. 0.059;
Matches 8; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

Qy 1 DCPSEWSSYEGFCYK 15
Db 12 DCPSDWYAYDQCYR 26

RESULT 13

US-09-870-759-95
; Sequence 95, Application US/09870759
; Patent No. US2002017551A1
; GENERAL INFORMATION:
; APPLICANT: TERMAN, David S
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
; FILE REFERENCE: 870759
; CURRENT APPLICATION NUMBER: US/09/870,759
; CURRENT FILING DATE: 2002-01-14
; PRIOR APPLICATION NUMBER: US 60/208,128
; PRIOR FILING DATE: 2000-05-30

Search completed: December 8, 2003, 10:07:05
Job time : 6.99429 secs

; NUMBER OF SEQ ID NOS: 166
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 95
; LENGTH: 1456
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-870-759-95

Query Match 56.5%; Score 61; DB 10; Length 1456;
Best Local Similarity 64.3%; Pred. No. 2.6;
Matches 9; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 2 CPSEWSSYEGFCYK 15
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Db 362 CPSQWPFYAGHCYK 375

RESULT 14
US-09-751-708A-95
; Sequence 95, Application US/09751708A
; Publication No. US20030157113A1
; GENERAL INFORMATION:
; APPLICANT: TERMAN, David S
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
; FILE REFERENCE: 751708
; CURRENT APPLICATION NUMBER: US/09/751,708A
; CURRENT FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: US 60/173,371
; PRIOR FILING DATE: 1999-12-28
; NUMBER OF SEQ ID NOS: 166
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 95
; LENGTH: 1456
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; ORGANISM: Homo sapiens
US-09-751-708A-95

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RESULT 15
US-09-764-870-302
; Sequence 302, Application US/09764870
; Patent No. US20020042386A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PTZ14
; CURRENT APPLICATION NUMBER: US/09/764,870
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 646
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 302
; LENGTH: 119
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-764-870-302

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Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 2 CPSEWSSYEGFCY 14
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Db 18 CPTSWLSFEGCY 30

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GenCore version 5.1.1.6
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Run on: December 8, 2003, 12:41:24 ; Search time 721.577 Seconds
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963.811 Million cell updates/sec

Title: US-09-938-114-4
Perfect score: 108
Sequence: 1 DCPSEWSYEGFCYKPF 17

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Fgapop 6.0 , Fgapext 7.0
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Searched: 2888711 seqs, 2045481386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	101	93.5	454	6	AR259041	Sequence
2	101	93.5	478	5	AY091756	Deinagkis
3	98	90.7	369	5	AY293866	Deinagkis
4	98	90.7	458	5	AF176421	Deinagkis
5	98	90.7	478	5	AY091761	Deinagkis
6	98	90.7	574	5	AF350324	Deinagkis
7	98	90.7	592	5	AB036881	Deinagkis
8	94	87.0	634	5	TFLFIXB	Trimeresuru
9	94	87.0	634	5	AF244901	Callosela
10	93	86.1	688	5	AF197915	Gloydus
11	86	79.6	664	5	AF540647	Deinagkis
12	84	77.8	583	5	AB019616	Deinagkis
13	83	76.9	690	6	AF125310	Agkistrod
14	83	76.9	690	6	AR026653	Gloydus
15	83	76.9	690	6	AX040807	Sequence
16	83	76.9	690	6	BD143687	Sequence
17	80	74.1	497	5	AY091758	Protein h
18	80	74.1	656	5	AB036880	Deinagkis
19	79	73.1	630	5	AF190827	Deinagkis
20	78	72.2	375	5	AF387100	Gloydus
21	78	72.2	483	6	AX427201	Deinagkis
22	78	72.2	484	5	AY091760	Sequence
23	77	71.3	733	5	AF176420	Deinagkis
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25	76	70.4	683	5	AB046491	Trimeresuru
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27	73	67.6	478	5	AY091755	Deinagkis
28	73	67.6	685	5	AF102902	Deinagkis
29	71	65.7	679	5	AB019615	Deinagkis
30	71	65.7	721	6	AX427204	Agkistrod
31	67	62.0	565	5	AY268948	Sequence
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33	66	61.1	487	5	AF463521	Deinagkis
34	66	61.1	488	5	AY091754	Deinagkis
35	66	61.1	580	6	AX427207	Deinagkis
36	66	61.1	619	5	AF40848	Sequence
37	66	61.1	704	5	AF102901	Deinagkis
38	64	59.3	170928	9	AF102901	Deinagkis
39	62	57.4	4040	5	AF325324	Xenopus l
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41	61	56.5	448	9	HUMANR07	Lactobacil
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						AL928590 Human DNA

ALIGNMENTS

RESULT 1

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AR259041
LOCUS AR259041 454 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 12 from patent US 6489451.
ACCESSION AR259041
VERSION AR259041.1 GI:27309526
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 454)
AUTHORS Li, B.X. and Cheng, X.
TITLE Antichromobis enzyme from the snake venom of agkistrodon acutus
JOURNAL Patent: US 6489451-A 12 03-DEC-2002;
FEATURES
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BASE COUNT 114 a 107 c 114 g 109 t 10 others
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Best Local Similarity: 94.12% Mismatches: 1
Query Match: 93.52% Indels: 0
DB: 6 Gaps: 0

US-09-938-114-4 (1-17) x AR259041 (1-454)

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Db 72 GATTGCTCCTGAGTGCTCTCTATGAGGGCATTGCTACAGCCCTTC 122

RESULT 2
LOCUS AR2591756 478 bp mRNA linear VRT 13-MAY-2002
DEFINITION Deinagkistrodon acutus clone 2100488 agkiscutacin B-chain mRNA,
complete cds.
ACCESSION AR2591756
VERSION AR2591756.1 GI:20562934
KEYWORDS Deinagkistrodon acutus
SOURCE Deinagkistrodon acutus
ORGANISM Deinagkistrodon acutus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Lepidodonta; Squamata; Scleroglossa; Serpentes; Colubroidea;
Viperidae; Crotalinae; Deinagkistrodon.
REFERENCE 1 (bases 1 to 478)
AUTHORS Yu, H., Xiang, K., Wang, Y. and Liu, J.
TITLE B chain of agkiscutacin from Deinagkistrodon acutus
JOURNAL Unpublished
AUTHORS Yu, H., Xiang, K., Wang, Y. and Liu, J.
TITLE Direct Submission
AUTHORS Submitted (22-MAR-2002) Dept. of Biochemistry and Molecular
JOURNAL Biology, University of Science and Technology of China, School of
Life Science, Huanqian Road, Hefei, Anhui 230027, P.R. China
FEATURES
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BASE COUNT 126 a 109 c 126 g 117 t
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Score: 101.00 Matches: 16
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Query Match: 93.52% Indels: 0
DB: 5 Gaps: 0

US-09-938-114-4 (1-17) x AY091756 (1-478)

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Db 70 GATTGCTCCTGAGTGCTCTCTATGAGGGCATTGCTACAGCCCTTC 120

RESULT 3
LOCUS AY293866 369 bp DNA linear VRT 09-JUN-2003
DEFINITION Deinagkistrodon acutus agkiscasin-b gene, partial cds.
ACCESSION AY293866
VERSION AY293866.1 GI:31559054
KEYWORDS Deinagkistrodon acutus
SOURCE Deinagkistrodon acutus
ORGANISM Deinagkistrodon acutus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Lepidodonta; Squamata; Scleroglossa; Serpentes; Colubroidea;
Viperidae; Crotalinae; Deinagkistrodon.
REFERENCE 1 (bases 1 to 369)
AUTHORS Zha, X.D., Ren, B., Liu, J. and Xu, K.S.
TITLE Genomic DNA sequence of b chain of Agkiscasin, a C-type lectin-like
protein from Agkistrodon acutus venom, and its evolutionary
significance
JOURNAL Unpublished
AUTHORS Zha, X.D., Ren, B., Liu, J. and Xu, K.S.
TITLE Direct Submission
JOURNAL Submitted (07-MAY-2003) Biology, School of Life Science, Anhui
University, 3 Peixi Road, Hefei 230039, China
FEATURES
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ORIGIN

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Score: 98.00 Matches: 15
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Query Match: 90.74% Indels: 0
DB: 5 Gaps: 0

US-09-938-114-4 (1-17) x AY293866 (1-369)

Qy 1 AspCysProSerGluTrpSerSerTyGluGlyPheCysTyrlsProphe 17
Db 1 GATTGCTCCTGAGTGCTCTCTATGAGGGCATTGCTACAGCCCTTC 51

RESULT 4
AF176421
    
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LOCUS AFI176421 458 bp mRNA linear VRT 19-JAN-2000
 DEFINITION Deinagkistrodon acutus agkiscutacin B chain mRNA, complete cds.
 ACCESSION AFI176421
 VERSION AFI176421.1 GI:6715114
 KEYWORDS
 SOURCE Deinagkistrodon acutus
 ORGANISM
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
 Viperidae; Crotalinae; Deinagkistrodon.
 REFERENCE 1 (bases 1 to 458)
 AUTHORS Cheng,X., Qian,X., Liu,Q., Li,B.X.Y., Ding,J., Xu,Z., Huang,W. and Liu,J.
 TITLE Agkiscutacin, a new fibrinolytic & anti-platelet protein from Agkistrodon acutus venom
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 458)
 AUTHORS Cheng,X., Liu,J., Li,B.X.Y. and Qian,Y.
 TITLE Direct Submission
 JOURNAL Submitted (08-AUG-1999) Dept. of Biochemistry and Molecular Biology, University of Science and Technology of China, School of Life-Science, Huangshan Road, Hefei, Anhui 230027, China
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 BASE COUNT 118 a 109 c 116 g 115 t
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 Pred. No.: 3.5e-07 Length: 458
 Score: 98.00 Matches: 15
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 Best Local Similarity: 88.24% Mismatches: 1
 Query Match: 90.74% Indels: 0
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 72 GATTGTCCTCTGATTGGTCTCTCTATGAAGGCGATTGCTACAGCCCTTC 122
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 AY091761
 LOCUS AY091761 478 bp mRNA linear VRT 13-MAY-2002
 DEFINITION Deinagkistrodon acutus clone 2101 ACF 1/2 B-chain mRNA, complete cds.
 ACCESSION AY091761
 VERSION AY091761.1 GI:20562942
 KEYWORDS
 SOURCE Deinagkistrodon acutus
 ORGANISM
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
 Viperidae; Crotalinae; Deinagkistrodon.
 REFERENCE 1 (bases 1 to 478)
 AUTHORS Yu,H., Xiang,K., Wang,Y. and Liu,J.
 TITLE B chain of ACF 1/2 from Deinagkistrodon acutus Unpublished

2 (bases 1 to 478)
 Yu,H., Xiang,K., Wang,Y. and Liu,J.
 Direct Submission
 Submitted (22-MAR-2002) Dept. of Biochemistry and Molecular Biology, University of Science and Technology of China, School of Life Science, Huangshan Road, Hefei, Anhui 230027, P.R. China
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 70 GATTGTCCTCTGATTGGTCTCTCTATGAAGGCGATTGCTACAGCCCTTC 120
 Db
 RESULT 6
 AF350324
 LOCUS AF350324 574 bp mRNA linear VRT 25-MAR-2001
 DEFINITION Deinagkistrodon acutus agkiscasin-b mRNA, complete cds.
 ACCESSION AF350324
 VERSION AF350324.1 GI:13445903
 KEYWORDS
 SOURCE Deinagkistrodon acutus
 ORGANISM
 Deinagkistrodon acutus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
 Viperidae; Crotalinae; Deinagkistrodon.
 REFERENCE 1 (bases 1 to 574)
 AUTHORS Zha,X. and Xu,K.
 TITLE Direct Submission
 JOURNAL Submitted (20-FEB-2001) Biochemical and Genetic Engineering Drugs, National Institute for Control of Pharmaceuticals and Biological Products, Tiantan Ximen, Xili Street 2, Beijing 10050, China
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 Score: 98.00 Matches: 15
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RESULT 7
 AB036881 592 bp mRNA linear VRT 23-MAY-2002
 LOCUS Deinagkistrodon acutus acp-b mRNA for anticoagulant protein-B,
 DEFINITION complete cds.

ACCESSION AB036881

VERSION AB036881.1 GI:12060180

KEYWORDS anticoagulant protein-B.

SOURCE Deinagkistrodon acutus

ORGANISM

Deinagkistrodon acutus
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
 Viperidae; Crotalinae; Deinagkistrodon.

REFERENCE

AUTHORS Tani,A., Ogawa,T., Nose,T., Nikandrov,N.N., Deshimaru,M.,

ChiJiwa,T., Chang,C.C., Fukumaki,Y. and Ohno,M.

TITLE Characterization, primary structure and molecular evolution of

anticoagulant protein from Agkistrodon actus venom

JOURNAL Toxicon 40 (6), 803-813 (2002)

MEDLINE 21975857

REFERENCE 2 (bases 1 to 592)

AUTHORS Ogawa,T. and Tani,A.

TITLE Direct Submission

JOURNAL Submitted (14-JAN-2000) Tomohisa Ogawa, Tohoku University, Graduate
 School of Agricultural Science; 1-1, Tsutsumidori Amamiyamachi,
 Aoba-ku, Sendai 981-8555, Japan (E-mail:ogawa@biochem.tohoku.ac.jp;
 URL:http://www.agri.tohoku.ac.jp/hoozo/, Tel:81-22-717-8808,
 Fax:81-22-717-8807)

FEATURES

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1. .592 /gene="acp-b"

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sig_peptide

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BASE COUNT 149 a 146 c 149 g 148 t

ORIGIN

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 Best Local Similarity: 88.24% Mismatches: 1
 Query Match: 90.74% Indels: 0
 DB: Gaps: 5

US-09-938-114-4 (1-17) x AB036881 (1-592)

QY 1 AspCysProSerGluTrpSerTyrGluGlyPheCysTyrIysProPhe 17
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 Db 74 GATTGCTCTGATTGGTCTCTTATGAAGGCGATTGCTACAGCCCTTC 124

RESULT 8

TFLEXB

LOCUS

DEFINITION

Trimeresurus flavoviridis mRNA for factor IX/factor X binding

protein B chain, complete cds.

ACCESSION D83332

VERSION D83332.1 GI:1402641

KEYWORDS factor IX/factor X binding protein B chain.

SOURCE Trimeresurus flavoviridis

ORGANISM

Trimeresurus flavoviridis
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 Lepidosauria; Squamata; Chordata; Serpentes; Colubroidea;
 Viperidae; Crotalinae; Trimeresurus.

REFERENCE 1 (bases 1 to 698)

AUTHORS Matsuzaki,R., Yoshiara,E., Yamada,M., Shima,K., Atoda,H. and

Morita,T.

TITLE cDNA cloning of IX/X-BP, a heterogeneous two-chain anticoagulant

protein from snake venom

JOURNAL Biochem. Biophys. Res. Commun. 220 (2), 382-387 (1996)

MEDLINE 96184662

PUBMED 8645314

REFERENCE 2 (bases 1 to 698)

AUTHORS Morita,T.

TITLE Direct Submission

JOURNAL Submitted (02-FEB-1996) Takashi Morita, Meiji College of Pharmacy,

Biochemistry; 1-22-1 Yatocho, Tanashi, Tokyo 188, Japan

(Tel:0424-21-0101(ex.429), Fax:0424-21-1489)

FEATURES

source

1. .698 /organism="Trimeresurus flavoviridis"

/mol_type="mRNA"

/db_xref="taxon:88087"

1. .773 /codon_start=1

74. .514 /product="factor IX/factor X binding protein B chain"

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/translation="MGRRFIFVSGFLVFLSLGTAADCPSDWSSYEGHCYKPFSEPK
 NWADAEFCTQHQHSHLVFSQSEADFVVKLAFQTFGHSIFWGLSNVWNCNQWQW
 SNAAMLKYDWAEESSYCVYFKSTNNKWSITCRMLANFVCEFOA"

3'UTR

polyA signal

BASE COUNT 167 a 185 c 177 g 169 t

ORIGIN

Alignment Scores:
 Pred. No.: 5,47e-07 Length: 698
 Score: 98.00 Matches: 15
 Percent Similarity: 94.12% Conservative: 1
 Best Local Similarity: 88.24% Mismatches: 1
 Query Match: 90.74% Indels: 0
 DB: Gaps: 5

US-09-938-114-4 (1-17) x TFLFIXB (1-698)

QY 1 AspCysProSerGluTrpSerTyrGluGlyPheCysTyrIysProPhe 17
 |||||:|||||

Db 143 GATTGCTCTGATTGGTCTCTTATGAAGGCGATTGCTACAGCCCTTC 193

RESULT 9

LOCUS

AF244901

DEFINITION

Calloselasma rhodostoma aggritin beta chain mRNA, partial cds.

ACCESSION AF244901

VERSION AF244901.1 GI:8809813

KEYWORDS

SOURCE

ORGANISM

Calloselasma rhodostoma (Malayan pit viper)

Calloselasma rhodostoma

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;

Viperidae; Crotalinae; Calloselasma.

1 (bases 1 to 438)

Chung, C.H., Au, L.C. and Huang, T.F.

Molecular cloning and sequence analysis of aggretin, a

collagen-like platelet aggregation inducer

Biochem. Biophys. Res. Commun. 263 (3), 723-727 (1999)

99443731

PUBMED

2 (bases 1 to 438)

Chung, C.H., Au, L.C. and Huang, T.F.

Direct Submission

Submitted (11-MAR-2000) Pharmacology, College of Medicine, National

Taiwan University, No. 1, Sec. 1, Jen-Ai Rd., Taipei, Taiwan

Location/Qualifiers

FEATURES

source

1..438

/organism="Calloselasma rhodostoma"

/mol_type="mRNA"

/db_xref="taxon:8717"

/tissue_type="venom gland"

1..>438

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collagen-receptor agonist; induces platelet aggregation;

similar to C-type lectins and glycoprotein Ib binding

proteins"

/codon_start=1

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/db_xref="GI:8809814"

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BASE COUNT

ORIGIN

108 a

100 c

121 g

109 t

Alignment Scores:

Pred. No.: 1..57e-06

Score: 94.00

Percent Similarity: 88.24%

Best Local Similarity: 88.24%

Query Match: 87.04%

DB: 5

Gaps: 0

US-09-938-114-4 (1-17) x AF244901 (1-438)

QY

Db

1

AspCysProSerGluTrpSerTyrGluGlyPheCysTyrIlysProphe 17

70

GATTGTCCTCTGGTGGTCTCTCTATGAAGGCATTGCTACAGCCCTTC 120

RESULT 10

AF197915

LOCUS

DEFINITION

AF197915

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

JOURNAL

source

FEATURES

source

1..634

/organism="Gloydius halys"

/mol_type="mRNA"

/db_xref="taxon:8714"

/tissue_type="venom"

24..464

/note="coagulation factor Xa inhibitor"

/codon_start=1

/product="halyxin B-chain precursor"

/protein_id="AAG28522.1"

/db_xref="GI:11066256"

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NWDAENFCTQQTGHLVSFHSSTEEADFYVKLAFQNFHGIFMMGLSNVWNCQSQW

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24..92

sig_peptide

mat_peptide

93..461

/product="halyxin B-chain"

BASE COUNT

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142 c

157 g

155 t

ORIGIN

Alignment Scores:

Pred. No.: 2.33e-06

Score: 94.00

Percent Similarity: 88.24%

Best Local Similarity: 88.24%

Query Match: 87.04%

DB: 5

Gaps: 0

US-09-938-114-4 (1-17) x AF197915 (1-634)

QY

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AspCysProSerGluTrpSerTyrGluGlyPheCysTyrIlysProphe 17

93

GATTGTCCTCTGGTGGTCTCTCTATGAAGGCATTGCTACAAACCATTT 143

RESULT 11

AF540647

LOCUS

DEFINITION

AF540647

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

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TITLE

JOURNAL

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JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

Submitted (22-OCT-1999) Cardiovascular center, Yonsei University
College of Med., 134 Shinchon-dong, Seoul 120-752, Republic of
Korea

Location/Qualifiers

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/organism="Gloydius halys"

/mol_type="mRNA"

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/tissue_type="venom"

24..464

/note="coagulation factor Xa inhibitor"

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/db_xref="GI:11066256"

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NWDAENFCTQQTGHLVSFHSSTEEADFYVKLAFQNFHGIFMMGLSNVWNCQSQW

SSAKLKYEAWEESYCVYFSTNNKRSACRMEAYFVCEPQA"

24..92

sig_peptide

mat_peptide

93..461

/product="halyxin B-chain"

BASE COUNT

180 a

142 c

157 g

155 t

ORIGIN

Alignment Scores:

Pred. No.: 2.33e-06

Score: 94.00

Percent Similarity: 88.24%

Best Local Similarity: 88.24%

Query Match: 87.04%

DB: 5

Gaps: 0

US-09-938-114-4 (1-17) x AF197915 (1-634)

QY

1

AspCysProSerGluTrpSerTyrGluGlyPheCysTyrIlysProphe 17

93

GATTGTCCTCTGGTGGTCTCTCTATGAAGGCATTGCTACAAACCATTT 143

RESULT 11

AF540647

LOCUS

DEFINITION

AF540647

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

Calloselasma rhodostoma (Malayan pit viper)

Calloselasma rhodostoma

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;

Viperidae; Crotalinae; Calloselasma.

1 (bases 1 to 438)

Chung, C.H., Au, L.C. and Huang, T.F.

Molecular cloning and sequence analysis of aggretin, a

collagen-like platelet aggregation inducer

Biochem. Biophys. Res. Commun. 263 (3), 723-727 (1999)

99443731

PUBMED

2 (bases 1 to 438)

Chung, C.H., Au, L.C. and Huang, T.F.

Direct Submission

Submitted (11-MAR-2000) Pharmacology, College of Medicine, National

Taiwan University, No. 1, Sec. 1, Jen-Ai Rd., Taipei, Taiwan

Location/Qualifiers

1..438

/organism="Calloselasma rhodostoma"

/mol_type="mRNA"

/db_xref="taxon:8717"

/tissue_type="venom gland"

1..>438

/note="forms heterodimer of alpha and beta chains;

collagen-receptor agonist; induces platelet aggregation;

similar to C-type lectins and glycoprotein Ib binding

proteins"

/codon_start=1

/product="aggretin beta chain"

/protein_id="AAF79953.1"

/db_xref="GI:8809814"

NWDAERFKIQPKHSLHVSFQAEADFYVKLTRPKANLVMMGLSLNIWHGCNQW

SDGARLNYKDWQSQCLAFRGVHTLWLNDCSTCSFVCKPKA"

BASE COUNT

108 a

100 c

121 g

109 t

Alignment Scores:

Pred. No.: 1.57e-06

Score: 94.00

Percent Similarity: 88.24%

Best Local Similarity: 88.24%

Query Match: 87.04%

DB: 5

Gaps: 0

US-09-938-114-4 (1-17) x AF244901 (1-438)

QY

1

AspCysProSerGluTrpSerTyrGluGlyPheCysTyrIlysProphe 17

70

GATTGTCCTCTGGTGGTCTCTCTATGAAGGCATTGCTACAGCCCTTC 120

RESULT 10

AF197915

LOCUS

DEFINITION

AF197915

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

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TWADAKFCTQOHKGHLASFHSSEADFWVLTTPSLKIDLVIWGLKNIWNGCYNWK
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61..129
sig_peptide
mat_peptide
130..498
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181 a 173 c 172 g 162 t
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Score: 93.00 Matches: 15
Percent Similarity: 88.24% Conservative: 0
Best Local Similarity: 88.24% Mismatches: 2
Query Match: 86.11% Indels: 0
DB: 5 Gaps: 0
US-09-938-114-4 (1-17) x AF540647 (1-688)
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Db 130 GATTGTCCTCTGAGTGGTCTCTCTATGAGGGCATTGCTACAGGCCTTC 180
RESULT 12
LOCUS AB019616 664 bp mRNA linear VRT 14-NOV-1998
DEFINITION Agkistrodon blomhoffi mRNA for mamushigin beta, complete cds.
ACCESSION AB019616
VERSION AB019616.1 GI:3882118
KEYWORDS mamushigin beta.
SOURCE Agkistrodon blomhoffi
ORGANISM Agkistrodon blomhoffi
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
Viperidae; Crotalinae; Agkistrodon.
1 (sites)
Sakurai, Y., Fujimura, Y., Kokubo, T., Imamura, K., Kawasaki, T.,
Handa, M., Suzuki, M., Matsui, T., Titani, K. and Yoshioka, A.
The cDNA cloning and molecular characterization of a snake venom
platelet glycoprotein Ib-binding protein, mamushigin, from
Agkistrodon halsys blomhoffii venom
Agkistrodon halsys blomhoffii
Thromb. Haemost. 79 (6), 1199-1207 (1998)
98319530
MEDLINE 9657448
PUBMED
REFERENCE 2 (bases 1 to 664)
Sakurai, Y. and Fujimura, Y.
Direct Submission
Submitted (10-NOV-1998) Yoshiniko Sakurai, Nara Medical University,
Department of Blood Transfusion Medicine, Shijo-cho 840, Kashihara,
Nara 634-8522, Japan (E-mail:ysakurai@nmu-gw.cc.naramed-u.ac.jp,
Tel:81-744-22-3051(ex.3288), Fax:81-744-29-0771)
Location/Qualifiers
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ORIGIN
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Pred. No.: 5.45e-05 Length: 664
Score: 86.00 Matches: 13
Percent Similarity: 88.24% Conservative: 2
Best Local Similarity: 76.47% Mismatches: 2
Query Match: 79.63% Indels: 0
DB: 5 Gaps: 0
US-09-938-114-4 (1-17) x AB019616 (1-664)
QY 1 AspCysProSerGluTrpSerSerTyrGluGlyPheCysTyrIysProPhe 17
Db 140 GATTGTCCTCTGATTGGTCTCTCTATGAGGGCATTGCTACAGGCCTTC 190
RESULT 13
LOCUS AF125310 583 bp mRNA linear VRT 04-MAR-1999
DEFINITION Gloydius halsys breviceaudus fibrinogen clotting inhibitor B chain
mRNA, complete cds.
ACCESSION AF125310
VERSION AF125310.1 GI:4337051
KEYWORDS Gloydius halsys breviceaudus
SOURCE Gloydius halsys breviceaudus
ORGANISM Gloydius halsys breviceaudus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
Viperidae; Crotalinae; Gloydius.
1 (bases 1 to 583)
Kim, D.S. and Koh, Y.S.
Purification and molecular cloning of snake venom fibrin clotting
inhibitor
Unpublished
REFERENCE 2 (bases 1 to 583)
Kim, D.S. and Koh, Y.S.
Direct Submission
Submitted (01-FEB-1999) Biochemistry, Yonsei University, Seodaemun
ku Shinchon dong 134, Seoul 120-749, Korea
Location/Qualifiers
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/notes="venom"
7..444
/notes="salmob"
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/protein_id="AADI8056.1"
/db_xref="GI:4337052"
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151 a 137 c 150 g 145 t
BASE COUNT 151 a 137 c 150 g 145 t
ORIGIN
Alignment Scores:
Pred. No.: 0.000103 Length: 583
Score: 84.00 Matches: 14
Percent Similarity: 82.35% Conservative: 0
Best Local Similarity: 82.35% Mismatches: 3
Query Match: 77.78% Indels: 0
DB: 5 Gaps: 0
US-09-938-114-4 (1-17) x AF125310 (1-583)
QY 1 AspCysProSerGluTrpSerSerTyrGluGlyPheCysTyrIysProPhe 17
Db 76 GATTGTCCTCTGTTGGTCTCTCTATGAGGGCATTGCTACAGGCCTTC 126

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RESULT 14
AR026653
LOCUS AR026653 690 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 7 from patent US 5856126.
ACCESSION AR026653
VERSION AR026653.1 GI:5937493
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
  1 (bases 1 to 690)
AUTHORS Fukuchi,N., Yamamoto,H., Nagano,M., Kito,M., Tanaka,A., Ishii,K.,
  Kobayashi,T. and Yoshimoto,R.
TITLE Peptide having anti-thrombus activity and method of producing the
  same
JOURNAL Patent: US 5856126-A 7 05-JAN-1999;
FEATURES
  Location/Qualifiers
    source
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BASE COUNT 167 a 180 c 170 g 173 t
ORIGIN

Alignment Scores:
Pred. No.: 0.000182 Length: 690
Score: 83.00 Matches: 12
Percent Similarity: 88.24% Conservative: 3
Best Local Similarity: 70.59% Mismatches: 2
Query Match: 76.85% Indels: 0
DB: 6 Gaps: 0

US-09-938-114-4 (1-17) x AR026653 (1-690)
QY 1 AspCysProSerGluTrpSerSerTyrrGluGlyPheCysTyrrLysProphe 17
Db 141 GAATGTCCTCCGGTGGTCTCTCTATGATCGGTATTGCTACAGCCCTTC 191

RESULT 15
AX404807
LOCUS AX404807 690 bp DNA linear PAT 14-JUN-2002
DEFINITION Sequence 2 from Patent EP1195384.
ACCESSION AX404807
VERSION AX404807.1 GI:21438046
KEYWORDS
SOURCE Crotalus horridus horridus
ORGANISM Crotalus horridus horridus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
Viperidae; Crotalinae; Crotalus.
REFERENCE
  1
AUTHORS Fukuchi,N.P., Kito,M.P., Kayahara,T.P., Futaki,F.P., Ishikawa,K.C.,
  Suzuki,E.C., Gondoh,K.C., Shimba,N.C. and Yamada,N.C.
TITLE Snake proteins having antithrombotic activity
JOURNAL Patent: EP 1195384-A 2 10-APR-2002;
FEATURES
  Location/Qualifiers
    source
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BASE COUNT 167 a 180 c 170 g 173 t
ORIGIN

Alignment Scores:

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Pred. No.: 0.000182 Length: 690
Score: 83.00 Matches: 12
Percent Similarity: 88.24% Conservative: 3
Best Local Similarity: 70.59% Mismatches: 2
Query Match: 76.85% Indels: 0
DB: 6 Gaps: 0

US-09-938-114-4 (1-17) x AX404807 (1-690)
QY 1 AspCysProSerGluTrpSerSerTyrrGluGlyPheCysTyrrLysProphe 17
Db 141 GAATGTCCTCCGGTGGTCTCTCTATGATCGGTATTGCTACAGCCCTTC 191

Search completed: December 8, 2003, 16:08:47
Job time : 723.577 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: December 8, 2003, 12:39:59 : Search time 58.3829 Seconds
(without alignments)
786.026 Million cell updates/sec

Title: US-09-938-114-4

Perfect score: 108

Sequence: 1 DCPSEWSSYEGFCVKPF 17

Scoring table:

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-LOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
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23: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA2001B.DAT.*
24: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA2002.DAT.*
25: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed,

and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	101	93.5	454	25	ABX93674	cDNA encoding Dein
2	94	87.0	633	22	AAI71877	Snake venom blood
3	84	77.8	583	24	AAL42016	Korean adder snake
4	83	76.9	690	16	AAQ89309	Snake venom anth
5	83	76.9	690	21	AAC61144	Snake venom anth
6	83	76.9	690	24	AAK99834	DNA encoding the a
7	79	73.1	601	22	AAI71876	Snake venom blood
8	78	72.2	483	24	AAD32053	Pigmy rattlesnake
9	71	65.7	721	24	AAD32055	Pigmy rattlesnake
10	66	61.1	453	24	AAD32054	Pigmy rattlesnake
11	66	61.1	580	24	AAD32057	Pigmy rattlesnake
12	61	56.5	1062	23	AAS84910	DNA encoding novel
13	61	56.5	5140	13	AAQ24977	DNA encoding solub
14	61	56.5	5457	23	AAS84913	DNA encoding novel
15	60	55.6	432	24	AAD32058	Pigmy rattlesnake
16	58	53.7	618	22	AAS31223	Human cDNA encodin
17	58	53.7	618	23	AAS73634	DNA encoding novel
18	58	53.7	618	24	ABQ66547	Human polynucleoti
19	58	53.7	632	24	AAL42015	Korean adder snake
20	58	53.7	825	22	AAK86241	Human immune/haema
21	58	53.7	900	24	AB211972	Human polynucleoti
22	58	53.7	1017	24	AB211973	Human polynucleoti
23	58	53.7	1355	20	AA234085	Human polynucleoti
24	58	53.7	1355	21	AAC78506	Human PRO792 nucle
25	58	53.7	1355	21	AAC58240	Human PRO792 nucle
26	58	53.7	1355	21	AAAT7635	Human PRO792 cDNA
27	58	53.7	1355	22	AA21454	Human cDNA sequenc
28	58	53.7	1355	25	ACA03813	Human cDNA encodin
29	58	53.7	1355	25	ACR04234	DNA encoding novel
30	58	53.7	1355	25	ABX89351	cDNA encoding huma
31	58	53.7	1355	25	ABX92457	Human immune/haema
32	58	53.7	1884	22	AAK86240	DNA encoding novel
33	57	52.8	621	24	ABK33326	Snake venom protei
34	57	52.8	716	17	AA674829	Pigmy rattlesnake
35	57	52.8	725	24	AAD32059	Human bone marrow
36	56.5	52.3	5624	22	AAH89920	Pigmy rattlesnake
37	56	51.9	456	24	ABD32058	Pigmy rattlesnake
38	55	50.9	443	25	ABX41898	Bovine EST associa
39	55	50.9	781	22	AAL00590	Human reproductive
40	55	50.9	1067	24	ABK88776	DNA encoding huma
41	55	50.9	1482	24	AAD28152	Human secretion an
42	55	50.9	1585	22	AAL03775	Human reproductive
43	55	50.9	1585	22	AAL03776	Human reproductive
44	55	50.9	5085	25	AB224622	Mouse macrophage m
45	54	50.0	857	22	AAS31230	Human cDNA encodin

ALIGNMENTS

RESULT 1
ABX93674

ID ABX93674 standard; cDNA; 454 BP.

XX AC ABX93674;

XX AC ABX93674;

DT 02-JUN-2003 (first entry)

XX cDNA encoding Deinagkistrodon acutus antithrombosis enzyme beta chain.

XX Antithrombosis; ss; PCR; beta chain; fibrin hydrolysis; blood clot;
XX platelet aggregation; vaso-occlusive disorder; thromboembolic disorder;
XX myocardial infarction; restenosis; cancer; neurodegenerative disease;
XX angiopathic thrombosis; cerebral thrombosis; thromboangiitis obliterans;
XX ischaemic cerebral vascular disease; unstable angina; acute thrombosis;
XX unstable stenocardia; pulmonary embolism; deep vein thrombosis; oedema;
XX peripheral arterial occlusion; stroke; atherosclerosis; inflammation;

KW thrombosis.

XX Deinagkistrodon acutus.

XX Key Location/Qualifiers

XX CDS 3..443

FT /*tag= a

FT /product= "Antithrombosis enzyme beta chain"

FT /transl_except= (pos:216..218,aa:Xaa)

FT /transl_except= (pos:219..221,aa:Xaa)

FT /transl_except= (pos:222..224,aa:Xaa)

FT /transl_except= (pos:225..227,aa:Xaa)

FT /note= "Xaa = unknown"

FT sig_peptide 3..71

FT /*tag= b

FT /note= "Leader peptide"

FT mat_peptide 72..440

FT /*tag= c

FT /note= "Mature beta chain"

FT misc_feature 217..226

FT /*tag= d

FT /note= "Unsequenced region could be 10-20 nucleotides in size"

XX US6489451-B1.

XX 03-DEC-2002.

XX 10-APR-1998; 98US-0058740.

XX 10-APR-1997; 97US-043886P.

XX (HEFE-) HEFEI SIU FUNG USTC PHARM CO LTD.

XX Li BX, Cheng X;

XX WPI; 2003-352116/33.

XX P-PSDB; ABU08799.

XX New purified Agkistrodon actus anti-thrombosis enzyme, useful for preventing and treating vaso-occlusive and thromboembolic disorders, including myocardial infarction, restenosis, cerebral thrombosis and unstable angina

XX Disclosure; Fig 1; 19pp; English.

XX The invention relates to a new Deinagkistrodon actus anti-thrombosis enzyme, where the enzyme hydrolyses fibrin, dissolves blood clots and prevents platelet aggregation. The anti-thrombosis enzyme was administered to rabbits intravenously. Thrombosis was determined before and after the administration at 0.5, 1.0, 2.0 and 3.0 hours by the Chandler method. The enzyme showed anti-thrombosis activity at 0.5 hour following administration at 0.005 micro/kg and this activity was increased significantly at 1.0 hour and at 0.01 micro /kg. The composition is useful for preventing and treating vaso-occlusive and thromboembolic disorders, including myocardial infarction, restenosis, angioathic thrombosis, cerebral thrombosis, ischaemic cerebral vascular diseases, unstable angina, acute thrombosis, unstable stenocardia, thromboangitis obliterans, pulmonary embolism, deep vein thrombosis, peripheral arterial occlusion, stroke. It is also useful for treating atherosclerosis, oedema and inflammation, cancer and neurodegenerative diseases. The present sequence represents cDNA encoding the Deinagkistrodon acutus antithrombosis enzyme beta chain.

XX Sequence 454 BP; 114 A; 107 C; 114 G; 109 T; 10 other;

Alignment Scores:

Pred. No.:	7,24e-07	Length:	454
Score:	101.00	Matches:	15
Percent Similarity:	94.12%	Conservative:	0
Best Local Similarity:	94.12%	Mismatches:	1
Query Match:	93.52%	Indels:	0
DB:	25	Gaps:	0

US-09-938-114-4 (1-17) x ABX93674 (1-454)

Qy 1 AspCysProSerGluTrpSerSerTyrGluGlyPheCysTyrLysProPhe 17

Db 72 GATTGTCCTCTGAGTGGTCTCTCTATGAAGGGCATTGCTACAAGCCCTTC 122

RESULT 2

AAI71877

ID AAI71877 standard; DNA; 633 BP.

XX AAI71877;

DT 10-JAN-2002 (first entry)

DE Snake venom blood anticoagulant halyxin B chain coding sequence.

KW Snake; pit viper; venom; halyxin; anticoagulant; thrombogenesis;

XX thrombosis; ds.

OS Agkistrodon halyx.

XX KR2001049671-A.

XX 15-JUN-2001.

XX 29-JUN-2000; 2000KR-0036591.

XX 29-JUN-1999; 99KR-0025105.

XX (BIOB-) BIOBUD CO LTD.

XX Jang YS, Jung GH, Kim DS, Koo BH, Son YD;

XX WPI; 2001-637330/73.

XX P-PSDB; AAM51544.

XX Halyxin as blood anticoagulation protein separated from snake venom - Claim 1; Page 11; 21pp; Korean.

XX The invention relates to halyxin, a novel protein with very strong blood anticoagulation activity. The protein was separated from snake venom of Agkistrodon halyx brevicaudus (a Korean pit viper) and can be used in the treatment of thrombogenesis. The present sequence encodes the B chain of halyxin.

XX Sequence 633 BP; 179 A; 142 C; 157 G; 155 T; 0 other;

Alignment Scores:

Pred. No.:	1,4e-05	Length:	633
Score:	94.00	Matches:	15
Percent Similarity:	88.24%	Conservative:	0
Best Local Similarity:	88.24%	Mismatches:	2
Query Match:	87.04%	Indels:	0
DB:	22	Gaps:	0

US-09-938-114-4 (1-17) x AAI71877 (1-633)

Qy 1 AspCysProSerGluTrpSerSerTyrGluGlyPheCysTyrLysProPhe 17

Db 93 GATTGTCCTCTGAGTGGTCTCTCTATGAAGGGCATTGCTACAACCATTT 143

RESULT 3

AAI42016

ID AAI42016 standard; cDNA; 583 BP.

XX AAI42016;

DT 16-MAY-2002 (first entry)

DE Korean adder snake venom salmorin B chain protein cDNA sequence.

XX

KW Korean adder; ss; salmorin protein B chain; snake venom;
 KW fibrinogen clotting inhibition; thrombosis; prothrombin binding;
 KW thrombin binding; blood coagulation.

OS Agkistrodon halys brevicaudus.

XX Key Location/Qualifiers
 XX CDS 7..444
 /*tag= a
 /product= "salmorin B chain protein"
 FT sig_peptide 7..75
 /*tag= b
 /note= "Signal peptide"
 FT mat_peptide 76..441
 /*tag= c
 /note= "Mature Salmorin B chain protein"
 FT 3'UTR 445..570
 /*tag= d
 FT polyA_signal 571..583
 /*tag= e

XX WO200214514-AL.

XX 21-FEB-2002.

XX 26-JUL-2001; 2001WO-KR01277.

XX 27-JUL-2000; 2000KR-0043470.

XX (BIOB-) BIOBUD CO LTD.

XX Chung K, Kim D, Koh Y;

XX WPI; 2002-241907/29.

XX P-PSDB; AAO14521.

XX New salmorin protein derived from venom of Korean adder Agkistrodon
 PT halys brevicaudus, useful for treating thrombosis by repressing
 PT fibrinogen clotting through repression of activation of prothrombin
 PT into thrombin

XX Claim 1; Fig 1B; 30pp; English.

XX The invention comprises the nucleotide and protein sequences of a
 CC salmorin protein derived from the venom of Korean adder. Salmorin protein
 CC is composed of an A chain and a B chain, and has inhibitory activity
 CC against fibrinogen clotting. The salmorin protein of the invention is
 CC useful for treating thrombosis, as it represses fibrinogen clotting
 CC potentially by binding to prothrombin and thrombin so as to delay blood
 CC coagulation. The present cDNA sequence encodes the Korean adder salmorin
 CC B chain protein.

XX SQ Sequence 583 BP; 151 A; 137 C; 150 G; 145 T; 0 other;

Alignment Scores:
 Pred. No.: 0.000487 Length: 583
 Score: 84.00 Matches: 14
 Percent Similarity: 82.35% Conservative: 0
 Best Local Similarity: 82.35% Mismatches: 3
 Query Match: 77.78% Indels: 0
 DB: 24 Gaps: 0

US-09-938-114-4 (1-17) x AAL42016 (1-583)

Qy 1 AspCysProSerGluTrpSerSerTyrGluGlyPheCysTyrIysProPhe 17
 Db 76 GAATGTCCTCGTGGTCTCTTATGAGGGCAATGCTACAGCTCTTC 126

RESULT 4
 AAQ89309

ID AAQ89309 standard; cDNA; 690 BP.

XX AC AAQ89309;

XX 25-MAR-2003 (updated)
 DT 28-NOV-1995 (first entry)
 XX Snake venom antithrombotic oligopeptide cDNA.
 XX Antithrombotic peptide; snake venom; platelet binding inhibition;
 KW von Willebrand factors; Crotalus horridus horridus; ds.
 XX Crotalus horridus horridus.

XX Key Location/Qualifiers
 XX CDS 66..515
 /*tag= a

XX WO9508573-AL.

XX 30-MAR-1995.

XX 21-SEP-1994; 94WO-JP01555.

XX 22-SEP-1993; 93JP-0236975.

XX (AJIN) AJINOMOTO KK.

XX Fukuchi N, Ishii K, Kito M, Kobayashi T, Nagano M;
 PI Tanaka A, Yamamoto H, Yoshimoto R;

XX WPI; 1995-139559/18.

XX P-PSDB; AAR71981.

XX Single-chain antithrombotic peptide - obtained by cleaving an
 PT oligopeptide from snake venom to break inter-chain di:sulphide
 PT bonds but preserve intra-chain di:sulphide bonds

XX Example 2; Pages 47-48; 84pp; Japanese.

XX AAR71978 and AAR71979 are snake venom derived antithrombotic peptides,
 CC specifically from the snake venom oligopeptide AAR71981, encoded by
 CC AAQ89309. These peptides have the advantage of avoiding significant
 CC thrombocytopenia when administered at the minimum dose, for in vivo
 CC inhibition of platelet von Willebrand factor binding.

XX (Updated on 25-MAR-2003 to correct PN field.)

XX SQ Sequence 690 BP; 167 A; 180 C; 170 G; 173 T; 0 other;

Alignment Scores:
 Pred. No.: 0.00086 Length: 690
 Score: 83.00 Matches: 12
 Percent Similarity: 88.24% Conservative: 3
 Best Local Similarity: 70.59% Mismatches: 2
 Query Match: 76.85% Indels: 0
 DB: 16 Gaps: 0

US-09-938-114-4 (1-17) x AAQ89309 (1-690)

Qy 1 AspCysProSerGluTrpSerSerTyrGluGlyPheCysTyrIysProPhe 17
 Db 141 GAATGTCCTCGTGGTCTCTTATGAGGGCAATGCTACAGCTCTTC 191

RESULT 5
 AAC61144

ID AAC61144 standard; DNA; 690 BP.

XX AC AAC61144;

XX 07-FEB-2001 (first entry)

XX DNA encoding a snake venom derived protein.

XX Subunit peptide production; snake venom; rattlesnake; thrombolytic;
 KW von Willebrand's factor; blood platelet-inhibitory activity; ds.

OS Crotalus horridus horridus.
XX WO200059926-A1.
XX 12-OCT-2000.
XX 31-MAR-2000; 2000WO-JP02127.
XX 02-APR-1999; 99JP-0096073.
XX (AJIN) AJINOMOTO CO INC.
XX Fukuchi N, Kageyama S, Kito M, Kayahara T, Yamamoto H;
XX WPI; 2000-664985/64.
XX P-PSDB; AAY85628.
XX Producing physiologically-active subunit peptides originating in
XX polymer proteins by denaturation and specific separation, with lower
XX antigenicity but improved solubility and stability, e.g. blood
XX platelet-binding inhibitors
XX Disclosure; Page 46; 51pp; Japanese.
XX This invention relates to a method for the production of a subunit
XX peptide originating from a polymer protein with disulphide bonds within
XX and between subunits. The method comprises denaturing the protein or its
XX subunit using a protein denaturing agent in a solution, removing the
XX agent in the presence of a polyoxyalkyl polyether which reacts with a
XX thiol group and unwinds the subunit, and separating the polyoxyalkyl
XX polyether-bound subunit peptide. The method can be used for producing
XX physiologically-active subunit peptides for polymer proteins e.g. snake
XX venom-originated dimer peptide with blood platelet-inhibitory activity
XX on von Willebrand's factor. The peptides produced have platelet-binding
XX inhibitory, and thrombolytic activity. The present sequence represents
XX DNA encoding rattlesnake protein used in an example illustrating the
XX method of the invention.
XX Sequence 690 BP; 167 A; 180 C; 170 G; 173 T; 0 other;
SQ

Alignment Scores:
Pred. No.: 0.00086 Length: 690
Score: 83.00 Matches: 12
Percent Similarity: 88.24% Conservative: 3
Best Local Similarity: 70.59% Mismatches: 2
Query Match: 76.85% Indels: 0
DB: 21 Gaps: 0

US-09-938-114-4 (1-17) x AAC61144 (1-690)
QY 1 AspCysProSerGluTyrSerSerTyrGluGlyPheCysTyrLysProphe 17
DB 141 GAATGTCCTCCGGTGGTCTCTCTATGATCGGTATGCTACAGCCCTTC 191

RESULT 6
AAK99834
ID AAK99834 standard; DNA; 690 BP.
AC AAK99834;
XX 19-JUL-2002 (first entry)
XX DNA encoding the antithrombotic wild-type rattlesnake protein.
XX Thrombolytic; glycoprotein Ib-binding protein; snake venom; rattlesnake;
XX antithrombotic; glycoprotein Ib; long half life; low antigenicity;
XX drug efficacy; gene; ds.
XX Crotalus horridus horridus.
XX Key Location/Qualifiers
FH 66..515
FT CDS /*tag= a
FT

/product= "Antithrombotic wild-type rattlesnake protein"
FT EPI195384-A1.
XX 10-APR-2002.
XX 04-OCT-2001; 2001EP-0123277.
XX 04-OCT-2000; 2000JP-0305279.
XX (AJIN) AJINOMOTO CO INC.
XX Fukuchi N, Kito M, Kayahara T, Futaki F, Ishikawa K, Suzuki E;
XX Gondeh K, Shimba N, Yamada N;
XX WPI; 2002-364482/40.
XX P-PSDB; AAO20974.
XX Glycoprotein Ib-binding protein, useful for treating thrombosis,
XX comprises specific mutations in protein originating from snake venom
XX Example 1; Page 25; 49pp; English.
XX The invention relates to a glycoprotein Ib-binding protein, originating
XX from snake venom, comprising specific mutations and antithrombotic
XX activity. Glycoprotein Ib-binding protein is used in a drug having
XX antithrombotic activity. Glycoprotein Ib-binding protein has a high
XX binding activity to glycoprotein Ib, a long half life/drug efficacy
XX retention in blood, and low antigenicity. This polynucleotide sequence
XX represents DNA of the wild-type rattlesnake protein of the invention.
XX Sequence 690 BP; 167 A; 180 C; 170 G; 173 T; 0 other;
SQ

Alignment Scores:
Pred. No.: 0.00086 Length: 690
Score: 83.00 Matches: 12
Percent Similarity: 88.24% Conservative: 3
Best Local Similarity: 70.59% Mismatches: 2
Query Match: 76.85% Indels: 0
DB: 24 Gaps: 0

US-09-938-114-4 (1-17) x AAK99834 (1-690)
QY 1 AspCysProSerGluTyrSerSerTyrGluGlyPheCysTyrLysProphe 17
DB 141 GAATGTCCTCCGGTGGTCTCTCTATGATCGGTATGCTACAGCCCTTC 191

RESULT 7
AAI71876
ID AAI71876 standard; DNA; 601 BP.
AC AAI71876;
XX 10-JAN-2002 (first entry)
XX Snake venom blood anticoagulant halyxin A chain coding sequence.
XX Snake; pit viper; venom; halyxin; anticoagulant; thrombogenesis;
XX thrombosis; ds.
XX Agkistrodon halys.
XX KR2001049671-A.
XX 15-JUN-2001.
XX 29-JUN-2000; 2000KR-0036591.
XX 29-JUN-1999; 99KR-0025105.
XX (BIOB-) BIOBUD CO LTD.
XX Jang YS, Jung GH, Kim DS, Koo BH, Son YD;
PI

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XX WPI: 2001-637330/73.
DR P-PSDB; AAM51543.
XX
XX Halyxin as blood anticoagulation protein separated from snake venom -
XX Claim 1; Page 9; 21pp; Korean.
XX
XX The invention relates to halyxin, a novel protein with very strong
XX blood anticoagulation activity. The protein was separated from snake
XX venom of Agkistrodon haly brevicaudus (a Korean pit viper) and can
XX be used in the treatment of thrombogenesis. The present sequence
XX encodes the A chain of halyxin.
XX
XX Sequence 601 BP; 166 A; 133 C; 163 G; 139 T; 0 other;
SQ
Alignment Scores:
Pred. No.: 0.00313 Length: 601
Score: 79.00 Matches: 13
Percent Similarity: 76.47% Conservative: 0
Best Local Similarity: 76.47% Mismatches: 4
Query Match: 73.15% Indels: 0
DB: 22 Gaps: 0
US-09-938-114-4 (1-17) x AAI71876 (1-601)
QY 1 AspCysProSerGluTrpSerSerTyrGluGlyPheCysTyrLysProPhe 17
DB 93 GATTGTCCCTCTGGTGGTCTCTCTATGAGGGCATTGCTACACATCTTC 143
RESULT 8
AAD32053
ID AAD32053 standard; DNA; 483 BP.
XX
XX AAD32053;
XX
XX 18-JUN-2002 (first entry)
XX
XX Pigmy rattlesnake venom gland protein, Zsnk2 gene.
XX
XX Pigmy rattlesnake; venom gland protein; blood coagulation; therapy;
XX platelet aggregation; gene; Zsnk2; ds.
XX
XX Sistrurus miliarius.
XX
XX Key Location/Qualifiers
XX CDS 3..458
XX /*tag= a
XX /product= "Zsnk2 protein"
XX /note= "CDS does not include start codon"
XX /partial
XX sig_peptide 3..59
XX /*tag= b
XX mat_peptide 60..455
XX /*tag= c
XX /product= "Mature Zsnk2 protein"
XX
XX WO200214364-A2.
XX
XX 21-FEB-2002.
XX
XX 13-AUG-2001; 2001WO-US25310.
XX
XX 14-AUG-2000; 2000US-225072P.
XX 14-AUG-2000; 2000US-225087P.
XX 15-AUG-2000; 2000US-225489P.
XX 15-AUG-2000; 2000US-225490P.
XX 20-DEC-2000; 2000US-356997P.
XX
XX (Zymo ) ZYMOGENETICS INC.
XX
XX Sheppard PO, Bishop PD;
XX
XX PF
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DR WPI: 2002-269180/31.
DR P-PSDB; AAE20178.
XX
XX New pigmy rattlesnake (Sistrurus miliarius) venom gland proteins, which
XX affect blood coagulation and platelet aggregation system, useful in
XX therapy and diagnostics, or as tools in the study of genetics or
XX molecular biology -
XX
XX Claim 5; Page 71-72; 79pp; English.
XX
XX The invention relates to new pigmy rattlesnake (Sistrurus miliarius)
XX venom gland proteins, which affect blood coagulation and platelet
XX aggregation system. The polypeptides, which affect blood coagulation and
XX platelet aggregation system, are useful in therapy and diagnostics. The
XX polypeptides are also useful as an educational tool in laboratory
XX practical kits for courses related to genetics and molecular biology,
XX protein chemistry and antibody production and analysis. The
XX polynucleotide or polypeptide can be used as standards or as unknowns
XX for testing purposes. The polypeptides are also useful in identifying
XX proteins by western blotting, protein purification, determining the
XX weight of expressed polypeptides as a ratio to total protein expressed,
XX identifying peptide cleavage sites, coupling amino and carboxyl terminal
XX tags, mass spectrometry, circular dichroism to determine conformation or
XX affinity chromatography columns to purify the protein, cloning or
XX sequencing. The present sequence is Sistrurus miliarius venom gland
XX protein, Zsnk2 gene.
XX
XX Sequence 483 BP; 129 A; 112 C; 123 G; 119 T; 0 other;
SQ
Alignment Scores:
Pred. No.: 0.00346 Length: 483
Score: 78.00 Matches: 12
Percent Similarity: 82.35% Conservative: 2
Best Local Similarity: 70.59% Mismatches: 3
Query Match: 72.22% Indels: 0
DB: 24 Gaps: 0
US-09-938-114-4 (1-17) x AAD32053 (1-483)
QY 1 AspCysProSerGluTrpSerSerTyrGluGlyPheCysTyrLysProPhe 17
DB 60 GATTGTCCCTCTGACCTGGTCTCTCTATGATCAGCATGCTACAGGCTCTTC 110
RESULT 9
AAD32055
ID AAD32055 standard; DNA; 721 BP.
XX
XX AAD32055;
XX
XX 18-JUN-2002 (first entry)
XX
XX Pigmy rattlesnake venom gland protein, Zsnk3 gene.
XX
XX Pigmy rattlesnake; venom gland protein; blood coagulation; therapy;
XX platelet aggregation; gene; Zsnk3; ds.
XX
XX Sistrurus miliarius.
XX
XX Key Location/Qualifiers
XX CDS 91..549
XX /*tag= a
XX /product= "Zsnk3 protein"
XX 91..159
XX sig_peptide /*tag= b
XX mat_peptide 160..546
XX /*tag= c
XX /product= "Mature Zsnk3 protein"
XX
XX WO200214364-A2.
XX
XX 21-FEB-2002.
XX
XX 13-AUG-2001; 2001WO-US25310.
XX
XX PF
```

XX 14-AUG-2000; 2000US-225072P.
 PR 14-AUG-2000; 2000US-225087P.
 PR 15-AUG-2000; 2000US-225489P.
 PR 15-AUG-2000; 2000US-225490P.
 PR 20-DEC-2000; 2000US-356997P.
 XX (ZYMO) ZYMOGENETICS INC.
 XX Sheppard PO, Bishop PD;
 XX WPI; 2002-269180/31.
 DR P-PSDB; AAE20179.
 XX New pigmy rattlesnake (Sistrurus miliarius) venom gland proteins, which
 PT affect blood coagulation and platelet aggregation system, useful in
 PT therapy and diagnostics, or as tools in the study of genetics or
 PT molecular biology -
 XX
 PS Claim 5; Page 73-74; 79pp; English.
 XX The invention relates to new pigmy rattlesnake (Sistrurus miliarius)
 CC venom gland proteins, which affect blood coagulation and platelet
 CC aggregation system. The polypeptides, which affect blood coagulation and
 CC platelet aggregation system, are useful in therapy and diagnostics. The
 CC polypeptides are also useful as an educational tool in laboratory
 CC practical kits for courses related to genetics and molecular biology,
 CC protein chemistry and antibody production and analysis. The
 CC polynucleotide or polypeptide can be used as standards or as unknowns
 CC for testing purposes. The polypeptides are also useful in identifying
 CC proteins by western blotting, protein purification, determining the
 CC weight of expressed polypeptides as a ratio to total protein expressed,
 CC identifying peptide cleavage sites, coupling amino and carboxyl terminal
 CC tags, mass spectrometry, circular dichroism to determine conformation or
 CC affinity chromatography columns to purify the protein, cloning or
 CC sequencing. The present sequence is Sistrurus miliarius venom gland
 CC protein, Zsnk3 gene.
 XX
 SQ Sequence 721 BP; 192 A; 167 C; 203 G; 159 T; 0 other;
 Alignment Scores:
 Pred. No.: 0.0725 Length: 721
 Score: 71.00 Matches: 11
 Percent Similarity: 76.47% Conservative: 2
 Best Local Similarity: 64.71% Mismatches: 4
 Query Match: 65.74% Indels: 0
 DB: 24 Gaps: 0
 US-09-938-114-4 (1-17) x AAD32055 (1-721)
 QY 1 AspCysProSerGluTrpSerSerTyrGluGlyPheCysTyrLysProPhe 17
 Db 160 GATTGCCCTGCTGGTGGTCTCTATGATCAGCATGTCACAGGCTTC 210
 RESULT 10
 AAD32054
 ID AAD32054 standard; DNA; 453 BP.
 XX
 AC AAD32054;
 XX
 DT 18-JUN-2002 (first entry)
 XX
 DE Pigmy rattlesnake venom gland protein Zsnk2, degenerate nucleic acid.
 XX
 KW Pigmy rattlesnake; venom gland protein; blood coagulation; therapy;
 KW platelet aggregation; ds.
 XX
 OS Sistrurus miliarius.
 XX
 PN WO200214364-A2.
 XX
 XX 21-FEB-2002.
 PD
 XX

PF 13-AUG-2001; 2001WO-US25310.
 XX
 PR 14-AUG-2000; 2000US-225072P.
 PR 14-AUG-2000; 2000US-225087P.
 PR 15-AUG-2000; 2000US-225489P.
 PR 15-AUG-2000; 2000US-225490P.
 PR 20-DEC-2000; 2000US-356997P.
 XX (ZYMO) ZYMOGENETICS INC.
 XX Sheppard PO, Bishop PD;
 XX WPI; 2002-269180/31.
 DR
 XX New pigmy rattlesnake (Sistrurus miliarius) venom gland proteins, which
 PT affect blood coagulation and platelet aggregation system, useful in
 PT therapy and diagnostics, or as tools in the study of genetics or
 PT molecular biology -
 XX
 PS Disclosure; Page 72-73; 79pp; English.
 XX The invention relates to new pigmy rattlesnake (Sistrurus miliarius)
 CC venom gland proteins, which affect blood coagulation and platelet
 CC aggregation system. The polypeptides, which affect blood coagulation and
 CC platelet aggregation system, are useful in therapy and diagnostics. The
 CC polypeptides are also useful as an educational tool in laboratory
 CC practical kits for courses related to genetics and molecular biology,
 CC protein chemistry and antibody production and analysis. The
 CC polynucleotide or polypeptide can be used as standards or as unknowns
 CC for testing purposes. The polypeptides are also useful in identifying
 CC proteins by western blotting, protein purification, determining the
 CC weight of expressed polypeptides as a ratio to total protein expressed,
 CC identifying peptide cleavage sites, coupling amino and carboxyl terminal
 CC tags, mass spectrometry, circular dichroism to determine conformation or
 CC affinity chromatography columns to purify the protein, cloning or
 CC sequencing. The present sequence is Sistrurus miliarius venom gland
 CC protein Zsnk2, degenerate nucleic acid.
 XX
 SQ Sequence 453 BP; 74 A; 32 C; 84 G; 70 T; 193 other;
 Alignment Scores:
 Pred. No.: 0.256 Length: 453
 Score: 66.00 Matches: 9
 Percent Similarity: 64.71% Conservative: 2
 Best Local Similarity: 52.94% Mismatches: 6
 Query Match: 61.11% Indels: 0
 DB: 24 Gaps: 0
 US-09-938-114-4 (1-17) x AAD32054 (1-453)
 QY 1 AspCysProSerGluTrpSerSerTyrGluGlyPheCysTyrLysProPhe 17
 Db 58 GAYTGYCCNWSNGAYTGGWSNNTAYGAYCARCAYTGYTAYARGNTTY 108
 RESULT 11
 AAD32057
 ID AAD32057 standard; DNA; 580 BP.
 XX
 AC AAD32057;
 XX
 DT 18-JUN-2002 (first entry)
 XX
 DE Pigmy rattlesnake venom gland protein, Zsnk4 gene.
 XX
 KW Pigmy rattlesnake; venom gland protein; blood coagulation; therapy;
 KW platelet aggregation; gene; Zsnk4; ds.
 XX
 OS Sistrurus miliarius.
 XX
 PH Key Location/Qualifiers
 FT CDS 3..437
 FT /*tag= a
 FT /product= "Zsnk4 protein"

XX AC AAQ24977;
 XX 25-MAR-2003 (updated)
 XX 18-NOV-1992 (first entry)
 XX DE DNA encoding soluble mannose receptor peptide.
 XX Soluble mannose receptor peptide; ss DNA; receptor binding;
 XX cancer cells; targeting; probe; drug delivery; cell marker;
 XX fusion molecule; AZT; ricin; pertussis; cholera toxin; liposome;
 XX therapeutic agent; diagnostic agent; opportunistic infections;
 XX immunocompromised patients; HIV.
 XX OS Homo sapiens.
 XX FH Key Location/Qualifiers
 XX FT CDS 59..4429
 XX FT /*tag= a
 XX PN WO9207579-A1.
 XX 14-MAY-1992.
 XX 06-NOV-1991; 91WO-US08320.
 XX 06-NOV-1990; 90US-0609915.
 XX (CHIL-) CHILDRENS MEDICAL CENT.
 XX Ezekowitz RAB;
 XX WPI; 1992-183410/22.
 XX P-PSDB; AAR24033.
 XX Soluble extracellular recombinant mannose receptor protein
 XX fragments - target mannose expressing cells for treatment and
 XX diagnosis of infections, cancer, etc.
 XX PS Disclosure; page 21-27; 37pp; English.
 XX The mannose receptor protein (MRP), or at least one carbohydrate
 XX recognition domain of it derived from an extracellular portion, can
 XX specifically bind pro- or eukaryotic pathogens, eg bacteria, fungi
 XX or viruses, with exposed configurations of mannose,
 XX N-acetylglucosamine or fucose on their cell wall or on the envelope
 XX glycoprotein. The protein lacks the MRP transmembrane and cytoplasmic
 XX regions and is capable of specifically targeting cells expressing the
 XX specified proteins. The MRPs can also target cancer cells which have
 XX any exposed mannose residues resulting from aberrant glycosylation.
 XX The proteins can be used as probes for such cells, or as fusion
 XX molecules for delivery of specific molecules, eg AZT, ricin, pertussis
 XX or cholera toxins, or CD4 to fix complement, or as an in vivo marker
 XX for immune system cells. The hybrid molecules are esp. capable of
 XX causing an effector molecule to be targeted to a cell, eg a virus.
 XX MRP and antibodies raised to it are also useful as therapeutic or
 XX diagnostic agents, eg for Leishmania protozoan parasites, Pneumocystis
 XX carinii, Candida albicans, Microbacterium tuberculosis, HIV or
 XX influenza virus. The antibodies are also useful to purify the MRP.
 XX The protein may be administered as a coating on a liposome, or as a
 XX powder or lotion.
 XX (Updated on 25-MAR-2003 to correct PN field.)
 XX SQ Sequence 5140 BP; 1598 A; 994 C; 1175 G; 1373 T; 0 other;
 Alignment Scores:
 Pred. No.: 30.3 Length: 5140
 Score: 61.00 Matches: 9
 Percent Similarity: 71.43% Conservativity: 1
 Best Local Similarity: 64.29% Mismatches: 4
 Query Match: 56.48% Indels: 0
 DB: 13 Gaps: 0

US-09-938-114-4 (1-17) x AAQ24977 (1-5140)
 QY 2 CysProSerGluTrpSerSerTyrGluGlyPheCysTyrLys 15
 DB 1142 TGTCCTAGTCAGTGGTGGCGGTATGCGGTCACTGTTACCAAG 1183
 RESULT 14
 AAS84913
 ID AAS84913 standard; cDNA; 5457 BP.
 XX AAS84913;
 XX DT 13-FEB-2002 (first entry)
 XX DE DNA encoding novel human diagnostic protein #20717.
 XX Human; chromosome mapping; gene mapping; gene therapy; forensic;
 XX food supplement; medical imaging; diagnostic; genetic disorder; ss.
 XX OS Homo sapiens.
 XX WO200175067-A2.
 XX 11-OCT-2001.
 XX 30-MAR-2001; 2001WO-US08631.
 XX 31-MAR-2000; 2000US-0540217.
 XX 23-AUG-2000; 2000US-0649167.
 XX (HYSE-) HYSEQ INC.
 XX Drmanac RT, Liu C, Tang YT;
 XX WPI; 2001-639362/73.
 XX P-PSDB; ABG20726.
 XX New isolated polynucleotide and encoded polypeptides, useful in
 XX diagnostics, forensics, gene mapping, identification of mutations
 XX responsible for genetic disorders or other traits and to assess
 XX biodiversity -
 XX Claim 1; SEQ ID No 20717; 103pp; English.
 XX The invention relates to isolated polynucleotide (I) and
 XX polypeptide (II) sequences. (I) is useful as hybridisation probes,
 XX polymerase chain reaction (PCR) primers, oligomers, and for chromosome
 XX and gene mapping, and in recombinant production of (II). The
 XX polynucleotides are also used in diagnostics as expressed sequence tags
 XX for identifying expressed genes. (I) is useful in gene therapy techniques
 XX to restore normal activity of (II) or to treat disease states involving
 XX (II). (II) is useful for generating antibodies against it, detecting or
 XX quantitating a polypeptide in tissue, as molecular weight markers and as
 XX a food supplement. (II) and its binding partners are useful in medical
 XX imaging of sites expressing (II). (I) and (II) are useful for treating
 XX disorders involving aberrant protein expression or biological activity.
 XX The polypeptide and polynucleotide sequences have applications in
 XX diagnostics, forensics, gene mapping, identification of mutations
 XX responsible for genetic disorders or other traits to assess biodiversity
 XX and to produce other types of data and products dependent on DNA and
 XX amino acid sequences. AAS64197-AAS94564 represent novel human
 XX diagnostic coding sequences of the invention.
 XX Note: The sequence data for this patent did not appear in the printed
 XX specification, but was obtained in electronic format directly from WIPO
 XX at ftp.wipo.int/pub/published_pct_sequences.
 XX SQ Sequence 5457 BP; 1645 A; 1081 C; 1276 G; 1455 T; 0 other;
 Alignment Scores:
 Pred. No.: 32.5 Length: 5457
 Score: 61.00 Matches: 9
 Percent Similarity: 71.43% Conservativity: 1
 Best Local Similarity: 64.29% Mismatches: 4

Query Match: 56.48% Indels: 0
 DB: 23 Gaps: 0
 US-09-938-114-4 (1-17) x AAS84913 (1-5457)
 Qy 2 CysProSerGluTrpSerSerTyrGluGlyPheCysTyrLys 15
 Db 1401 TGTCTAGTCAGTGGTGGCCGTATGCCGTCACCTGTACAG 1442

RESULT 15

AAD32058
 ID AAD32058 standard; DNA; 432 BP.
 XX
 AC AAD32058;
 XX
 DT 18-JUN-2002 (first entry)
 XX
 DE Pigmy rattlesnake venom gland protein Zsnk4, degenerate nucleic acid.
 XX
 KW Pigmy rattlesnake; venom gland protein; blood coagulation; therapy;
 KW platelet aggregation; ds.
 XX
 OS Sistrurus miliarius.

XX
 FN WO200214364-A2.

XX
 PD 21-FEB-2002.

XX
 PF 13-AUG-2001; 2001WO-US25310.

XX
 PR 14-AUG-2000; 2000US-225072P.

PR 14-AUG-2000; 2000US-225087P.

PR 15-AUG-2000; 2000US-225489P.

PR 15-AUG-2000; 2000US-225490P.

PR 20-DEC-2000; 2000US-356997P.

XX
 PA (ZYMO) ZYMOGENETICS INC.

XX
 PI Sheppard PO, Bishop PD;

XX
 DR WPI; 2002-269180/31.

XX
 PT New pigmy rattlesnake (Sistrurus miliarius) venom gland proteins, which
 PT affect blood coagulation and platelet aggregation system, useful in
 PT therapy and diagnostics, or as tools in the study of genetics or
 PT molecular biology

XX
 PS Disclosure; Page 76; 79pp; English.

XX
 CC The invention relates to new pigmy rattlesnake (Sistrurus miliarius)
 CC venom gland proteins, which affect blood coagulation and platelet
 CC aggregation system. The polypeptides, which affect blood coagulation and
 CC platelet aggregation system, are useful in therapy and diagnostics. The
 CC polypeptides are also useful as an educational tool in laboratory
 CC practical kits for courses related to genetics and molecular biology,
 CC protein chemistry and antibody production and analysis. The
 CC polynucleotide or polypeptide can be used as standards or as unknowns
 CC for testing purposes. The polypeptides are also useful in identifying
 CC proteins by western blotting, protein purification, determining the
 CC weight of expressed polypeptides as a ratio to total protein expressed,
 CC identifying peptide cleavage sites, coupling amino and carboxyl terminal
 CC tags, mass spectrometry, circular dichroism to determine conformation or
 CC affinity chromatography columns to purify the protein, cloning or
 CC sequencing. The present sequence is Sistrurus miliarius venom gland
 CC protein Zsnk4, degenerate nucleic acid.

XX
 SQ Sequence 432 BP; 91 A; 34 C; 84 G; 55 T; 168 other;

Alignment Scores:

Align. No.: 2.16 Length: 432
 Score: 60.00 Matches: 7
 Percent Similarity: 78.57% Conservative: 4
 Best Local Similarity: 50.00% Mismatches: 3

Query Match: 55.56% Indels: 0
 DB: 24 Gaps: 0
 US-09-938-114-4 (1-17) x AAD32058 (1-432)
 Qy 1 AspCysProSerGluTrpSerSerTyrGluGlyPheCysTyr 14
 Db 34 GAYTGCCNWSNGAYTGGTAYGCNTAYGAYCARTAYTGTAY 75

Search completed: December 8, 2003, 14:04:49
 Job time : 60.3829 secs

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GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: December 8, 2003, 13:49:04 ; Search time 13.4057 Seconds
(without alignments)
559.725 Million cell updates/sec

Title: US-09-938-114-4

Perfect score: 108

Sequence: 1 DCFSEWSSYRGFCVKPF 17

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-Q/cgn2_1/USPRO.spool/US0938114/runat_08122003_091001_22878/app_query.fasta_1.725

-DB=Issued Patents NA -QFMT=fastap -SUFFIX=rni -MINMATCH=0.1 -LOOPEL=0

-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS-human4.0.cdi

-LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15

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-NO MAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG

-DRV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6

-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued Patents NA.*

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5: /cgn2_6/ptodata/1/ina/PTCUS COMB.seq.*

6: /cgn2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	101	93.5	454	4	US-09-058-740-12
2	83	76.9	690	2	Sequence 12, Appl
3	54	50.0	1600	4	Sequence 7, Appl
4	52	48.1	360	3	Sequence 1, Appl
5	52	48.1	405	3	Sequence 4, Appl
6	52	48.1	405	3	Sequence 3, Appl
7	52	48.1	645	3	Sequence 7, Appl
8	52	48.1	693	3	Sequence 12, Appl
9	52	48.1	699	3	Sequence 13, Appl
10	52	48.1	1212	3	Sequence 11, Appl
11	52	48.1	1212	3	Sequence 9, Appl
12	52	48.1	1212	3	Sequence 10, Appl
					Sequence 11, Appl

13	52	48.1	1222	3	US-08-543-246B-5	Sequence 5, Appl
14	52	48.1	1223	4	US-09-016-434-1347	Sequence 1347, Ap
15	52	48.1	1312	4	US-09-517-605-1	Sequence 1, Appl
16	52	48.1	1333	3	US-08-543-246B-15	Sequence 15, Appl
17	52	48.1	1387	3	US-08-543-246B-1	Sequence 1, Appl
18	52	48.1	1643	4	US-09-517-605-16	Sequence 16, Appl
19	51	47.2	1764	2	US-08-504-459-3	Sequence 3, Appl
20	51	47.2	3259	5	PCT-US95-03747-1	Sequence 1, Appl
21	50	46.3	216	4	US-09-016-434-583	Sequence 583, App
22	50	46.3	5169	4	US-09-194-612A-2	Sequence 2, Appl
23	50	46.3	11225	6	5182210-9	Patent No. 5182210
24	49	45.4	1422	3	US-08-867-611-25	Sequence 25, Appl
25	49	45.4	1422	5	PCT-US92-06965A-30	Sequence 30, Appl
26	49	45.4	2076	4	US-09-489-847-51	Sequence 51, Appl
27	49	45.4	9401	2	US-08-432-693-1	Sequence 1, Appl
28	49	45.4	9416	3	US-08-811-566-19	Sequence 19, Appl
29	49	45.4	9416	4	US-09-034-756-19	Sequence 19, Appl
30	49	45.4	124884	4	US-09-661-596A-76	Sequence 76, Appl
31	48	44.4	402	3	US-08-543-246B-10	Sequence 10, Appl
32	48	44.4	558	2	US-08-896-365-5	Sequence 5, Appl
33	48	44.4	648	3	US-08-543-246B-14	Sequence 14, Appl
34	48	44.4	1755	3	US-08-543-246B-8	Sequence 8, Appl
35	48	44.4	1806	4	US-09-252-991A-1534	Sequence 1534, Ap
36	48	44.4	2376	2	US-08-760-745-4	Sequence 4, Appl
37	48	44.4	3843	4	US-09-252-991A-1430	Sequence 1430, Ap
38	48	44.4	5337	4	US-09-252-991A-1588	Sequence 1588, Ap
39	47	43.5	152	3	US-08-772-440-40	Sequence 40, Appl
40	47	43.5	393	3	US-08-772-440-22	Sequence 22, Appl
41	47	43.5	501	3	US-08-772-440-20	Sequence 20, Appl
42	47	43.5	600	5	PCT-US93-10418-3	Sequence 3, Appl
43	47	43.5	1104	3	US-09-111-470-1	Sequence 1, Appl
44	47	43.5	1227	3	US-08-772-440-3	Sequence 3, Appl
45	47	43.5	2045	3	US-08-743-168B-42	Sequence 42, Appl

ALIGNMENTS

RESULT 1

US-09-058-740-12

; Sequence 12, Application US/09058740

; Patent No. 6489451

; GENERAL INFORMATION:

; APPLICANT: Chun Wang, Benjamin XY Li, Xin Cheng,

; Jing Liu, Li-Wen Niu, Wan-Zhi Huang,

; Zhen-Yu Xu, Dan Luo, Lian-Di Kang,

; Jin-Guo Ding, Fang Rong, Yan Liu and

; Hui-Ran Chen

; TITLE OF INVENTION: AN ANTITHROMBOSIS ENZYME FROM THE SNAKE

; CORRESPONDENCE ADDRESS: VENOM OF AGKISTRODON ACUTUS

; NUMBER OF SEQUENCES: 12

; ADDRESS: Lyon & Lyon

; STREET: 633 West Fifth Street

; CITY: Suite 4700

; STATE: California

; COUNTRY: U.S.A.

; ZIP: 90071-2066

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: IBM P.C. DOS 5.0

; SOFTWARE: FastSeq for Windows 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/058,740

; FILING DATE: 10-Apr-1998

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: <Unknown>

; FILING DATE: <Unknown>

; ATTORNEY/AGENT INFORMATION:

; NAME: Chen, Anthony C.

REGISTRATION NUMBER: 38,673
REFERENCE/DOCKET NUMBER: 233/298
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 454 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY: Coding Sequence
LOCATION: 3...440
OTHER INFORMATION: "N" stands for any base.
"Xaa" stands for any amino acid.
SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-09-058-740-12

Alignment Scores:
Pred. No.: 3,26e-08 Length: 454
Score: 101.00 Matches: 16
Percent Similarity: 94.12% Conservative: 0
Best Local Similarity: 94.12% Mismatches: 1
Query Match: 93.52% Indels: 0
DB: 4 Gaps: 0

US-09-938-114-4 (1-17) x US-09-058-740-12 (1-454)

QY 1 AspCysProSerGluTrpSerSerTyrrGluGlyPheCysTyrIlysProphe 17
Db 72 GAATGTCCTCTGAGTGGTCTCTCTATGAAGGGCATGCTACAGCCCTTC 122

RESULT 2
US-08-612-840A-7
Sequence 7, Application US/08612840A
Patent No. 5856126
GENERAL INFORMATION:
APPLICANT: FUKUCHI, Naoyuki
APPLICANT: YAMAMOTO, Hiroshi
APPLICANT: NAGANO, Mitsuyo
APPLICANT: KITO, Morikazu
APPLICANT: TANAKA, Akiko
APPLICANT: ISHII, Koichi
APPLICANT: KOBAYASHI, Tsuyoshi
APPLICANT: YOSHIMOTO, Ryota
TITLE OF INVENTION: PEPTIDE HAVING ANTI-THROMBUS ACTIVITY AND
TITLE OF INVENTION: METHOD OF PRODUCING THE SAME
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Obion, Spivak, McClelland, Maier & Neustadt, P.C.
STREET: 1755 S. Jefferson Davis Highway, Suite 400
CITY: Arlington
STATE: VA
COUNTRY: USA
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/612,840A
FILING DATE: 20-MAR-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 5-236975
FILING DATE: 22-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: No. 5856126man F. Obion
REGISTRATION NUMBER: 24,618
TELECOMMUNICATION INFORMATION:

TELEPHONE: 703-413-3000
TELEFAX: 703-413-2220
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 690 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Crotaulus horridus horridus
STRAIN:
FEATURE:
NAME/KEY: CDS
LOCATION: 56..512
US-08-612-840A-7

Alignment Scores:
Pred. No.: 5,53e-05 Length: 690
Score: 83.00 Matches: 12
Percent Similarity: 88.24% Conservative: 3
Best Local Similarity: 70.59% Mismatches: 2
Query Match: 76.85% Indels: 0
DB: 2 Gaps: 0

US-09-938-114-4 (1-17) x US-08-612-840A-7 (1-690)

QY 1 AspCysProSerGluTrpSerSerTyrrGluGlyPheCysTyrIlysProphe 17
Db 141 GAATGTCCTCCGGTTGGTCTCTCTATGATCGGTATTGCTACAGCCCTTC 191

RESULT 3
US-09-585-228-1
Sequence 1, Application US/09585228
Patent No. 6531576
GENERAL INFORMATION:
APPLICANT: Piddington, Christopher S.
APPLICANT: West, James W.
APPLICANT: HOLLY, Richard D.
APPLICANT: Burkhead, Steven K.
TITLE OF INVENTION: FOUR-HELICAL BUNDLE PROTEIN ZSIG81
FILE REFERENCE: 99-13
CURRENT APPLICATION NUMBER: US/09/585,228
CURRENT FILING DATE: 2000-06-01
EARLIER APPLICATION NUMBER: US 60/137,057
EARLIER FILING DATE: 1999-06-01
NUMBER OF SEQ ID NOS: 36
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 1
LENGTH: 1600
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (134)...(655)
NAME/KEY: sig_peptide
LOCATION: (134)...(184)
US-09-585-228-1

Alignment Scores:
Pred. No.: 10.9 Length: 1600
Score: 54.00 Matches: 7
Percent Similarity: 61.54% Conservative: 1
Best Local Similarity: 53.85% Mismatches: 5
Query Match: 50.00% Indels: 0
DB: 4 Gaps: 0

US-09-938-114-4 (1-17) x US-09-585-228-1 (1-1600)

QY 2 CysProSerGluTrpSerSerTyrrGluGlyPheCysTyr 14
Db 141 GAATGTCCTCCGGTTGGTCTCTCTATGATCGGTATTGCTACAGCCCTTC 191

Db 1420 TGCCCGAGCTCTGGCACCATTATTCGCTTCTGTTT 1458

RESULT 4
US-08-543-246B-4
; Sequence 4, Application US/08543246B
; Patent No. 6262244
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: DNA and amino acid sequence specific for
; TITLE OF INVENTION: natural killer cells
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Michael W. Glynn
; ADDRESSEE: No. 6262244artis Corporation
; STREET: 564 Morris Avenue
; CITY: Summit,
; STATE: NJ
; COUNTRY: US
; ZIP: 07901-1027
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/543,246B
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/676,663
; FILING DATE: 28-MAR-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/02469
; FILING DATE: 27-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/122,514
; FILING DATE: 24-SEP-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Kassenoff, Melvyn M.
; REGISTRATION NUMBER: 26,389
; REFERENCE/DOCKET NUMBER: 118-7704/PCT/CONT
; TELEPHONE: 908-522-6927
; TELEFAX: 908-522-6955
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 360 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; US-08-543-246B-4

Alignment Scores:
Pred. No.: 3 61 Length: 360
Score: 52.00 Matches: 7
Percent Similarity: 61.54% Conservative: 1
Best Local Similarity: 53.85% Mismatches: 5
Query Match: 48.15% Indels: 0
DB: 3 Gaps: 0

US-09-938-114-4 (1-17) x US-08-543-246B-4 (1-360)

QY 2 CysProSerGluTrpSerSerTyrGluGlyPheCysTyr 14
||||| :|||
Db 16 TGTCCTGAGAGTGGATTACATATTCACACAGTTGTTAC 54

RESULT 5
US-08-543-246B-3
; Sequence 3, Application US/08543246B
; Patent No. 6262244
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: DNA and amino acid sequence specific for
; TITLE OF INVENTION: natural killer cells
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Michael W. Glynn
; ADDRESSEE: No. 6262244artis Corporation
; STREET: 564 Morris Avenue
; CITY: Summit,
; STATE: NJ
; COUNTRY: US
; ZIP: 07901-1027
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/543,246B
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/676,663
; FILING DATE: 28-MAR-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/02469
; FILING DATE: 27-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/122,514
; FILING DATE: 24-SEP-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Kassenoff, Melvyn M.
; REGISTRATION NUMBER: 26,389
; REFERENCE/DOCKET NUMBER: 118-7704/PCT/CONT
; TELEPHONE: 908-522-6927
; TELEFAX: 908-522-6955
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 360 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; US-08-543-246B-4

Alignment Scores:
Pred. No.: 3 61 Length: 360
Score: 52.00 Matches: 7
Percent Similarity: 61.54% Conservative: 1
Best Local Similarity: 53.85% Mismatches: 5
Query Match: 48.15% Indels: 0
DB: 3 Gaps: 0

US-09-938-114-4 (1-17) x US-08-543-246B-4 (1-360)

QY 2 CysProSerGluTrpSerSerTyrGluGlyPheCysTyr 14
||||| :|||
Db 16 TGTCCTGAGAGTGGATTACATATTCACACAGTTGTTAC 54

RESULT 6
US-08-543-246B-7
; Sequence 7, Application US/08543246B
; Patent No. 6262244
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: DNA and amino acid sequence specific for
; TITLE OF INVENTION: natural killer cells
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Michael W. Glynn
; ADDRESSEE: No. 6262244artis Corporation

; APPLICANT:
; TITLE OF INVENTION: DNA and amino acid sequence specific for
; TITLE OF INVENTION: natural killer cells
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Michael W. Glynn
; ADDRESSEE: No. 6262244artis Corporation
; STREET: 564 Morris Avenue
; CITY: Summit,
; STATE: NJ
; COUNTRY: US
; ZIP: 07901-1027
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/543,246B
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/676,663
; FILING DATE: 28-MAR-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/02469
; FILING DATE: 27-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/122,514
; FILING DATE: 24-SEP-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Kassenoff, Melvyn M.
; REGISTRATION NUMBER: 26,389
; REFERENCE/DOCKET NUMBER: 118-7704/PCT/CONT
; TELEPHONE: 908-522-6927
; TELEFAX: 908-522-6955
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 405 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; US-08-543-246B-3

Alignment Scores:
Pred. No.: 4 18 Length: 405
Score: 52.00 Matches: 7
Percent Similarity: 61.54% Conservative: 1
Best Local Similarity: 53.85% Mismatches: 5
Query Match: 48.15% Indels: 0
DB: 3 Gaps: 0

US-09-938-114-4 (1-17) x US-08-543-246B-3 (1-405)

QY 2 CysProSerGluTrpSerSerTyrGluGlyPheCysTyr 14
||||| :|||
Db 61 TGTCCTGAGAGTGGATTACATATTCACACAGTTGTTAC 99

RESULT 6
US-08-543-246B-7
; Sequence 7, Application US/08543246B
; Patent No. 6262244
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: DNA and amino acid sequence specific for
; TITLE OF INVENTION: natural killer cells
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Michael W. Glynn
; ADDRESSEE: No. 6262244artis Corporation

STREET: 564 Morris Avenue
CITY: Summit,
STATE: NJ
COUNTRY: US
ZIP: 07901-1027
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/543,246B
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/676,663
FILING DATE: 28-MAR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/02469
FILING DATE: 27-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/122,514
FILING DATE: 24-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: Kassenoff, Melvyn M.
REGISTRATION NUMBER: 26,389
REFERENCE/DOCKET NUMBER: 118-7704/PCT/CONT
TELEPHONE: 908-522-6927
TELEFAX: 908-522-6955
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 405 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-543-246B-7

Alignment Scores:
Pred. No.: 4.18 Length: 405
Score: 52.00 Matches: 7
Percent Similarity: 61.54% Conservative: 1
Best Local Similarity: 53.85% Mismatches: 5
Query Match: 48.15% Indels: 0
DB: 3 Gaps: 0

US-09-938-114-4 (1-17) x US-08-543-246B-7 (1-405)

QY 2 CysProSerGluTrpSerSerTyrGluGlyPheCysTyr 14
Db 61 TGTCTGAGGAGTGGATTACATATCCACAGTTGTAT 99

RESULT 7
US-08-543-246B-12
Sequence 12, Application US/08543246B
Patent No. 6262244
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: DNA and amino acid sequence specific for
TITLE OF INVENTION: natural killer cells
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Michael W. Glyn
ADDRESSEE: No. 6262244artis Corporation
STREET: 564 Morris Avenue
CITY: Summit,
STATE: NJ
COUNTRY: US
ZIP: 07901-1027
COMPUTER READABLE FORM: disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/543,246B
FILING DATE:
PRIOR APPLICATION DATA:

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/543,246B
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/676,663
FILING DATE: 28-MAR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/02469
FILING DATE: 27-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/122,514
FILING DATE: 24-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: Kassenoff, Melvyn M.
REGISTRATION NUMBER: 26,389
REFERENCE/DOCKET NUMBER: 118-7704/PCT/CONT
TELEPHONE: 908-522-6927
TELEFAX: 908-522-6955
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 645 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-543-246B-12

Alignment Scores:
Pred. No.: 7.5 Length: 645
Score: 52.00 Matches: 7
Percent Similarity: 61.54% Conservative: 1
Best Local Similarity: 53.85% Mismatches: 5
Query Match: 48.15% Indels: 0
DB: 3 Gaps: 0

US-09-938-114-4 (1-17) x US-08-543-246B-12 (1-645)

QY 2 CysProSerGluTrpSerSerTyrGluGlyPheCysTyr 14
Db 301 TGTCTGAGGAGTGGATTACATATCCACAGTTGTAT 339

RESULT 8
US-08-543-246B-13
Sequence 13, Application US/08543246B
Patent No. 6262244
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: DNA and amino acid sequence specific for
TITLE OF INVENTION: natural killer cells
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Michael W. Glyn
ADDRESSEE: No. 6262244artis Corporation
STREET: 564 Morris Avenue
CITY: Summit,
STATE: NJ
COUNTRY: US
ZIP: 07901-1027
COMPUTER READABLE FORM: disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/543,246B
FILING DATE:
PRIOR APPLICATION DATA:

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; APPLICATION NUMBER: US 07/676,663
; FILING DATE: 28-MAR-1991
; PRIOR APPLICATION DATA: PCT/US92/02469
; APPLICATION NUMBER: PCT/US92/02469
; FILING DATE: 27-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/122,514
; FILING DATE: 24-SEP-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Kassenoff, Melvyn M.
; REGISTRATION NUMBER: 26,389
; REFERENCE/DOCKET NUMBER: 118-7704/PCT/CONT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 908-522-6927
; TELEFAX: 908-522-6955
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 693 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; US-08-543-246B-13

Alignment Scores:
Pred. No.: 8.2 Length: 693
Score: 52.00 Matches: 7
Percent Similarity: 61.54% Conservative: 1
Best Local Similarity: 53.85% Mismatches: 5
Query Match: 48.15% Indels: 0
DB: 3 Gaps: 0

US-09-938-114-4 (1-17) x US-08-543-246B-13 (1-693)

QY 2 CysProSerGluTrpSerSerTyrGluGlyPheCysTyr 14
Db 349 TGTCCTGAGAGTGGATTACATATCCACAGTTGTAT 387

RESULT 9
US-08-543-246B-11
; Sequence 11, Application US/08543246B
; Patent No. 6262244
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: DNA and amino acid sequence specific for
; TITLE OF INVENTION: natural killer cells
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Michael W. Glynn
; ADDRESSEE: No. 6262244artis Corporation
; STREET: 564 Morris Avenue
; CITY: Summit,
; STATE: NJ
; COUNTRY: US
; ZIP: 07901-1027
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/543,246B
; FILING DATE:
; PRIOR APPLICATION DATA:
; PRIOR APPLICATION NUMBER: US 07/676,663
; FILING DATE: 28-MAR-1991
; PRIOR APPLICATION DATA:
; PRIOR APPLICATION NUMBER: PCT/US92/02469
; FILING DATE: 27-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/122,514
```

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; FILING DATE: 24-SEP-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Kassenoff, Melvyn M.
; REGISTRATION NUMBER: 26,389
; REFERENCE/DOCKET NUMBER: 118-7704/PCT/CONT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 908-522-6927
; TELEFAX: 908-522-6955
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 699 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; US-08-543-246B-11

Alignment Scores:
Pred. No.: 8.29 Length: 699
Score: 52.00 Matches: 7
Percent Similarity: 61.54% Conservative: 1
Best Local Similarity: 53.85% Mismatches: 5
Query Match: 48.15% Indels: 0
DB: 3 Gaps: 0

US-09-938-114-4 (1-17) x US-08-543-246B-11 (1-699)

QY 2 CysProSerGluTrpSerSerTyrGluGlyPheCysTyr 14
Db 355 TGTCCTGAGAGTGGATTACATATCCACAGTTGTAT 393

RESULT 10
US-09-591-435-9
; Sequence 9, Application US/09591435
; Patent No. 6280953
; GENERAL INFORMATION:
; APPLICANT: MESSIER, WALTER
; APPLICANT: SIKELA, JAMES M
; TITLE OF INVENTION: METHODS TO IDENTIFY POLYNUCLEOTIDE AND POLYPEPTIDE
; TITLE OF INVENTION: SEQUENCES WHICH MAY BE ASSOCIATED WITH PHYSIOLOGICAL
; TITLE OF INVENTION: AND MEDICAL CONDITIONS
; FILE REFERENCE: GENO.200.2
; CURRENT APPLICATION NUMBER: US/09/591,435
; PRIOR FILING DATE: 2000-06-09
; PRIOR APPLICATION NUMBER: 09/591,435
; PRIOR FILING DATE: 2000-06-09
; PRIOR APPLICATION NUMBER: 09/240,915
; PRIOR FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: 60/073,263
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: 60/098,987
; PRIOR FILING DATE: 1998-09-02
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 1212
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-591-435-9

Alignment Scores:
Pred. No.: 16.5 Length: 1212
Score: 52.00 Matches: 7
Percent Similarity: 76.92% Conservative: 3
Best Local Similarity: 53.85% Mismatches: 3
Query Match: 48.15% Indels: 0
DB: 3 Gaps: 0

US-09-938-114-4 (1-17) x US-09-591-435-9 (1-1212)

QY 2 CysProSerGluTrpSerSerTyrGluGlyPheCysTyr 14
```

	US-09-591-435-11	Alignment Scores:	Pred. No.: 16.5	Length: 1212
		Score:	52.00	Matches: 7
		Percent Similarity:	76.92%	Conservative: 3
		Best Local Similarity:	53.85%	Mismatches: 3
		Query Match:	48.15%	Indels: 0
		DB:	3	Gaps: 0
	US-09-938-114-4 (1-17) x US-09-591-435-11 (1-1212)			
QY	2 CysProSerGluTrpSerSerTyrGluGlyPheCysTyr 14			
Db	766 TGCCCTGGGAATGGACATTCTCCAAGAAACTGTTC 804			
	RESULT 13			
	US-08-543-246B-5			
	; Sequence 5, Application US/08543246B			
	; Patent No. 6262244			
	; GENERAL INFORMATION:			
	; APPLICANT:			
	; TITLE OF INVENTION: DNA and amino acid sequence specific for			
	; TITLE OF INVENTION: natural killer cells			
	; NUMBER OF SEQUENCES: 24			
	; CORRESPONDENCE ADDRESS:			
	; ADDRESSEE: Michael W. Glynn			
	; ADDRESSEE: No. 6262244artis Corporation			
	; STREET: 564 Morris Avenue			
	; CITY: Summit,			
	; STATE: NJ			
	; COUNTRY: US			
	; ZIP: 07901-1027			
	; COMPUTER READABLE FORM:			
	; MEDIUM TYPE: Floppy disk			
	; COMPUTER: IBM PC compatible			
	; OPERATING SYSTEM: PC-DOS/MS-DOS			
	; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)			
	; CURRENT APPLICATION DATA:			
	; APPLICATION NUMBER: US/08/543,246B			
	; FILING DATE:			
	; PRIOR APPLICATION DATA:			
	; APPLICATION NUMBER: US 07/676,663			
	; FILING DATE: 28-MAR-1991			
	; PRIOR APPLICATION DATA:			
	; APPLICATION NUMBER: PCT/US92/02469			
	; FILING DATE: 27-MAR-1992			
	; PRIOR APPLICATION DATA:			
	; APPLICATION NUMBER: US 08/122,514			
	; FILING DATE: 24-SEP-1993			
	; ATTORNEY/AGENT INFORMATION:			
	; NAME: Kassenoff, Melvyn M.			
	; REGISTRATION NUMBER: 26,389			
	; REFERENCE/DOCKET NUMBER: 118-7704/PCT/CONT			
	; TELECOMMUNICATION INFORMATION:			
	; TELEPHONE: 908-522-6927			
	; TELEFAX: 908-522-6955			
	; INFORMATION FOR SEQ ID NO: 5:			
	; SEQUENCE CHARACTERISTICS:			
	; LENGTH: 1222 base pairs			
	; TYPE: nucleic acid			
	; STRANDEDNESS: double			
	; TOPOLOGY: linear			
	; MOLECULE TYPE: DNA (genomic)			
	; HYPOTHEetical: NO			
	; ANTI-SENSE: NO			
	; FEATURE:			
	; NAME/KEY: CDS			
	; LOCATION: 8..700			
	; FEATURE:			
	; NAME/KEY: mat_peptide			
	; LOCATION: 8..700			
	US-08-543-246B-5			

	US-09-591-435-11	Alignment Scores:	Pred. No.: 16.5	Length: 1212
		Score:	52.00	Matches: 7
		Percent Similarity:	76.92%	Conservative: 3
		Best Local Similarity:	53.85%	Mismatches: 3
		Query Match:	48.15%	Indels: 0
		DB:	3	Gaps: 0
	US-09-938-114-4 (1-17) x US-09-591-435-10 (1-1212)			
QY	2 CysProSerGluTrpSerSerTyrGluGlyPheCysTyr 14			
Db	766 TGCCCTGGGAATGGACATTCTCCAAGAAACTGTTC 804			
	RESULT 12			
	US-09-591-435-11			
	; Sequence 11, Application US/09591435			
	; Patent No. 6280953			
	; GENERAL INFORMATION:			
	; APPLICANT: MESSIER, WALTER			
	; APPLICANT: SIKELA, JAMES M			
	; TITLE OF INVENTION: METHODS TO IDENTIFY POLYNUCLEOTIDE AND POLYPEPTIDE			
	; TITLE OF INVENTION: SEQUENCES WHICH MAY BE ASSOCIATED WITH PHYSIOLOGICAL			
	; FILE REFERENCE: GENO.200.2			
	; CURRENT APPLICATION NUMBER: US/09/591,435			
	; CURRENT FILING DATE: 2000-06-09			
	; PRIOR APPLICATION NUMBER: 09/591,435			
	; PRIOR FILING DATE: 2000-06-09			
	; PRIOR APPLICATION NUMBER: 09/240,915			
	; PRIOR FILING DATE: 1999-01-29			
	; PRIOR APPLICATION NUMBER: 60/073,263			
	; PRIOR FILING DATE: 1998-01-30			
	; PRIOR APPLICATION NUMBER: 60/098,987			
	; PRIOR FILING DATE: 1998-09-02			
	; NUMBER OF SEQ ID NOS: 13			
	; SOFTWARE: PatentIn Ver. 2.0			
	; SEQ ID NO 10			
	; LENGTH: 1212			
	; TYPE: DNA			
	; ORGANISM: Pan troglodytes			
	US-09-591-435-10			

	US-09-591-435-11	Alignment Scores:	Pred. No.: 16.5	Length: 1212
		Score:	52.00	Matches: 7
		Percent Similarity:	76.92%	Conservative: 3
		Best Local Similarity:	53.85%	Mismatches: 3
		Query Match:	48.15%	Indels: 0
		DB:	3	Gaps: 0
	US-09-938-114-4 (1-17) x US-09-591			

Alignment Scores:
Pred. No.: 16.7 Length: 1222
Score: 52.00 Matches: 7
Percent Similarity: 61.54% Conservative: 1
Best Local Similarity: 53.85% Mismatches: 5
Query Match: 48.15% Indels: 0
DB: 3 Gaps: 0

US-09-938-114-4 (1-17) x US-08-543-246B-5 (1-1222)

Qy 2 CysProSerGluTrpSerSerTyrGluGlyPheCysTyr 14
Db 356 TGCTCTGAGGAGTGATTACATATTCACACAGTTGTTAT 394
||||| ||||| :|||
RESULT 14
US-09-016-434-1347
; Sequence 1347, Application US/09016434
; Patent No. 6500938
; GENERAL INFORMATION:
; APPLICANT: Janice Au-Young
; APPLICANT: Jeffrey J. Sellhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
; TITLE OF INVENTION: PATHWAY GENE EXPRESSION
; NUMBER OF SEQUENCES: 1490
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/016,434
; FILING DATE: HEREWITH
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0002 US
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 1347:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1223 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GENBANK
; CLONE: G35060
US-09-016-434-1347

Alignment Scores:
Pred. No.: 16.7 Length: 1223
Score: 52.00 Matches: 7
Percent Similarity: 61.54% Conservative: 1
Best Local Similarity: 53.85% Mismatches: 5
Query Match: 48.15% Indels: 0
DB: 4 Gaps: 0

US-09-938-114-4 (1-17) x US-09-016-434-1347 (1-1223)

Qy 2 CysProSerGluTrpSerSerTyrGluGlyPheCysTyr 14
Db 356 TGCTCTGAGGAGTGATTACATATTCACACAGTTGTTAT 394
||||| ||||| :|||
RESULT 15
US-09-517-605-1
; Sequence 1, Application US/09517605
; Patent No. 6391567
; GENERAL INFORMATION:
; APPLICANT: Littman, Dan R.
; APPLICANT: Kwon, Douglas S.
; APPLICANT: van Kooyk, Yvette
; APPLICANT: Geijtenbeek, Theo
; TITLE OF INVENTION: METHODS OF USING A FACILITATOR OF RETROVIRAL ENTRY INTO
; TITLE OF INVENTION: CELLS
; FILE REFERENCE: 1049-1-017
; CURRENT APPLICATION NUMBER: US/09/517,605
; CURRENT FILING DATE: 2000-03-02
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 1312
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (42)..(1253)
US-09-517-605-1

Alignment Scores:
Pred. No.: 18.3 Length: 1312
Score: 52.00 Matches: 7
Percent Similarity: 76.92% Conservative: 3
Best Local Similarity: 53.85% Mismatches: 3
Query Match: 48.15% Indels: 0
DB: 4 Gaps: 0

US-09-938-114-4 (1-17) x US-09-517-605-1 (1-1312)

Qy 2 CysProSerGluTrpSerSerTyrGluGlyPheCysTyr 14
Db 807 TGCTCTGAGGAGTGATTACATATTCACACAGTTGTTAT 845
||||| ||||| :|||

Search completed: December 8, 2003, 17:27:05
Job time : 15.4057 secs

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GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: December 8, 2003, 16:08:50 ; Search time 67.6114 Seconds
(without alignments)
835.675 Million cell updates/sec

Title: US-09-938-114-4

Perfect score: 108

Sequence: 1 DCPSEWSYEGFCYKPF 17

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2201672 segs, 1661799599 residues

Total number of hits satisfying chosen parameters: 4403344

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODE=frame+ p2n.model -DRV=xlh
-Q=/cgn2_1/USPTO.spool/US0938114/runat_08122003_091002_22963/app_query.fasta_1.725
-DB=Published Applications NA -QFMT=FastCap -SUFFIX=rnpb -MINMATCH=0.1
-LOOPCL=0 -LOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62
-TRANS-human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100
-THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0
-MAXLEN=2000000000 -USER=US0938114.ecgn 1_1_504_runat_08122003_091002_22963
-NCPUS=6 -ICPU=3 -NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100
-LONGLOG -DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published Applications NA:

1:	/cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:
2:	/cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:
3:	/cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:
4:	/cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:
5:	/cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:
6:	/cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:
7:	/cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:
8:	/cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:
9:	/cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq:
10:	/cgn2_6/ptodata/2/pubpna/US09H_PUBCOMB.seq:
11:	/cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:
12:	/cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:
13:	/cgn2_6/ptodata/2/pubpna/US09A_NEW_PUB.seq:
14:	/cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:
15:	/cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:
16:	/cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:
17:	/cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:
18:	/cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description

1	83	76.9	690	10	US-09-969-763-2	Sequence 2, Appli
2	78	72.2	483	10	US-09-929-230-1	Sequence 1, Appli
3	78	72.2	483	13	US-10-226-420-1	Sequence 1, Appli
4	71	65.7	721	10	US-09-929-230-4	Sequence 4, Appli
5	71	65.7	721	13	US-10-226-420-4	Sequence 4, Appli
6	66	61.1	453	10	US-09-929-230-3	Sequence 3, Appli
7	66	61.1	453	13	US-10-226-420-3	Sequence 3, Appli
8	66	61.1	580	10	US-09-929-230-7	Sequence 7, Appli
9	66	61.1	580	13	US-10-226-420-7	Sequence 7, Appli
10	61	56.5	5185	10	US-09-870-759-94	Sequence 94, Appli
11	61	56.5	5185	13	US-09-751-708A-9	Sequence 94, Appli
12	60	55.6	432	10	US-09-929-230-9	Sequence 9, Appli
13	60	55.6	432	13	US-10-226-420-9	Sequence 9, Appli
14	58	53.7	618	9	US-09-764-870-37	Sequence 37, Appli
15	58	53.7	618	15	US-10-125-540-37	Sequence 37, Appli
16	58	53.7	1355	10	US-09-978-295A-230	Sequence 230, App
17	58	53.7	1355	10	US-09-978-697-230	Sequence 230, App
18	58	53.7	1355	10	US-09-978-192A-230	Sequence 230, App
19	58	53.7	1355	10	US-09-999-832A-230	Sequence 230, App
20	58	53.7	1355	11	US-09-978-189-230	Sequence 230, App
21	58	53.7	1355	11	US-09-978-608A-230	Sequence 230, App
22	58	53.7	1355	11	US-09-978-585A-230	Sequence 230, App
23	58	53.7	1355	11	US-09-978-191A-230	Sequence 230, App
24	58	53.7	1355	11	US-09-978-403A-230	Sequence 230, App
25	58	53.7	1355	11	US-09-978-564A-230	Sequence 230, App
26	58	53.7	1355	11	US-09-999-833A-230	Sequence 230, App
27	58	53.7	1355	11	US-09-981-915A-230	Sequence 230, App
28	58	53.7	1355	11	US-09-978-824-230	Sequence 230, App
29	58	53.7	1355	11	US-09-918-585A-230	Sequence 230, App
30	58	53.7	1355	11	US-09-978-423A-230	Sequence 230, App
31	58	53.7	1355	11	US-09-978-193A-230	Sequence 230, App
32	58	53.7	1355	11	US-09-999-830A-230	Sequence 230, App
33	58	53.7	1355	11	US-09-978-757A-230	Sequence 230, App
34	58	53.7	1355	11	US-09-978-187B-230	Sequence 230, App
35	58	53.7	1355	11	US-09-978-643A-230	Sequence 230, App
36	58	53.7	1355	13	US-09-978-375A-230	Sequence 230, App
37	58	53.7	1355	13	US-09-978-188A-230	Sequence 230, App
38	58	53.7	1355	13	US-09-978-298A-230	Sequence 230, App
39	58	53.7	1355	13	US-10-137-870-421	Sequence 421, App
40	58	53.7	1355	13	US-10-140-018-421	Sequence 421, App
41	58	53.7	1355	13	US-10-140-021-421	Sequence 421, App
42	58	53.7	1355	13	US-10-140-274-421	Sequence 421, App
43	58	53.7	1355	13	US-10-140-471-421	Sequence 421, App
44	58	53.7	1355	13	US-10-140-807-421	Sequence 421, App
45	58	53.7	1355	13	US-10-140-922-421	Sequence 421, App

ALIGNMENTS

RESULT 1
US-09-969-763-2
; Sequence 2, Application US/09969763
; Publication No. US20020198363A1
; GENERAL INFORMATION:
; APPLICANT: FUKUCHI, NAOYUKI
; APPLICANT: KITO, MORIKAZU
; APPLICANT: KAYAHARA, TAKASHI
; APPLICANT: FUTAKI, FUMIE
; APPLICANT: ISHIKAWA, KOHKI
; APPLICANT: SUZUKI, EIICHIRO
; APPLICANT: GONDOH, KEIKO
; APPLICANT: SHIMBA, NOBUHISA
; APPLICANT: YAMADA, NAOYUKI
; TITLE OF INVENTION: PROTEIN HAVING ANTITHROMBOTIC ACTIVITY AND METHOD FOR PRODUCING IT
; FILE REFERENCE: 214760US0
; CURRENT APPLICATION NUMBER: US/09/969, 763
; CURRENT FILING DATE: 2000-10-25
; PRIOR APPLICATION NUMBER: JP 2000-305279
; PRIOR FILING DATE: 2000-10-04
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 690

; TYPE: DNA
; ORGANISM: Crotalus harridus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (66)..(512)
; OTHER INFORMATION:
US-09-969-763-2

Alignment Scores:
Pred. No.: 7.15e-05 Length: 690
Score: 83.00 Matches: 12
Percent Similarity: 88.24% Conservatives: 3
Best Local Similarity: 70.59% Mismatches: 2
Query Match: 76.85% Indels: 0
DB: 10 Gaps: 0

US-09-938-114-4 (1-17) x US-09-969-763-2 (1-690)

Qy 1 AspCysProSerGluTrpSerTyrGluGlyPheCysTyrLysProphe 17
Db 141 GAATGCCCCCTCGGTGGTCTCTATGATCGGTATGCTACAGCCCTTC 191

RESULT 2

US-09-929-230-1
; Sequence 1, Application US/09929230
; Patent No. US20020161203A1
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Bishop, Paul D.
; TITLE OF INVENTION: RATTLESNAKE VENOM GLAND PROTEINS
; FILE REFERENCE: 00-72
; CURRENT APPLICATION NUMBER: US/09/929,230
; CURRENT FILING DATE: 2001-08-13
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1

; LENGTH: 483
; TYPE: DNA
; ORGANISM: Sistrurus miliarius
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (3)...(455)
; NAME/KEY: misc feature
; LOCATION: (0)..(0)
; OTHER INFORMATION: Zsnk2
US-09-929-230-1

Alignment Scores:
Pred. No.: 0.000342 Length: 483
Score: 78.00 Matches: 12
Percent Similarity: 82.35% Conservatives: 2
Best Local Similarity: 70.59% Mismatches: 3
Query Match: 72.22% Indels: 0
DB: 10 Gaps: 0

US-09-938-114-4 (1-17) x US-09-929-230-1 (1-483)

Qy 1 AspCysProSerGluTrpSerTyrGluGlyPheCysTyrLysProphe 17
Db 60 GATTGCCCCCTGACTGGTCTCTATGATCAGCATGCTACAGGCTTC 110

RESULT 3

US-10-226-420-1
; Sequence 1, Application US/10226420
; Publication No. US20030157686A1
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Bishop, Paul D.
; TITLE OF INVENTION: RATTLESNAKE VENOM GLAND PROTEINS
; FILE REFERENCE: 00-72
; CURRENT APPLICATION NUMBER: US/10/226,420
; CURRENT FILING DATE: 2002-08-21
; NUMBER OF SEQ ID NOS: 14

; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 483
; TYPE: DNA
; ORGANISM: Sistrurus miliarius
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (3)...(455)
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (0)..(0)
; OTHER INFORMATION: Zsnk2
US-10-226-420-1

Alignment Scores:
Pred. No.: 0.000342 Length: 483
Score: 78.00 Matches: 12
Percent Similarity: 82.35% Conservatives: 2
Best Local Similarity: 70.59% Mismatches: 3
Query Match: 72.22% Indels: 0
DB: 13 Gaps: 0

US-09-938-114-4 (1-17) x US-10-226-420-1 (1-483)

Qy 1 AspCysProSerGluTrpSerTyrGluGlyPheCysTyrLysProphe 17
Db 60 GATTGCCCCCTGACTGGTCTCTATGATCAGCATGCTACAGGCTTC 110

RESULT 4

US-09-929-230-4
; Sequence 4, Application US/09929230
; Patent No. US20020161203A1
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Bishop, Paul D.
; TITLE OF INVENTION: RATTLESNAKE VENOM GLAND PROTEINS
; FILE REFERENCE: 00-72
; CURRENT APPLICATION NUMBER: US/09/929,230
; CURRENT FILING DATE: 2001-08-13
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4

; LENGTH: 721
; TYPE: DNA
; ORGANISM: Sistrurus miliarius
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (91)...(546)
; NAME/KEY: misc feature
; LOCATION: (0)..(0)
; OTHER INFORMATION: Zsnk3
US-09-929-230-4

Alignment Scores:
Pred. No.: 0.00873 Length: 721
Score: 71.00 Matches: 11
Percent Similarity: 76.47% Conservatives: 2
Best Local Similarity: 64.71% Mismatches: 4
Query Match: 65.74% Indels: 0
DB: 10 Gaps: 0

US-09-938-114-4 (1-17) x US-09-929-230-4 (1-721)

Qy 1 AspCysProSerGluTrpSerTyrGluGlyPheCysTyrLysProphe 17
Db 160 GATTGCCCCCTGCTGCTCTATGATCAGCATGCTACAGGCTTC 210

RESULT 5

US-10-226-420-4
; Sequence 4, Application US/10226420
; Publication No. US20030157686A1
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.

```

; APPLICANT: Bishop, Paul D.
; TITLE OF INVENTION: RATTLESNAKE VENOM GLAND PROTEINS
; FILE REFERENCE: 00-72
; CURRENT APPLICATION NUMBER: US/10/226,420
; CURRENT FILING DATE: 2002-08-21
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 721
; TYPE: DNA
; ORGANISM: Sistrurus miliarius
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (91)...(546)
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: Zsnk3
US-10-226-420-4
Alignment Scores:
Pred. No.: 0.00873          Length: 721
Score: 71.00              Matches: 11
Percent Similarity: 76.47%  Conservative: 2
Best Local Similarity: 64.71% Mismatches: 4
Query Match: 65.74%        Indels: 0
DB: 13                    Gaps: 0
US-09-938-114-4 (1-17) x US-10-226-420-4 (1-721)
QY 1 AspCysProSerGluTrpSerSerTyrGluGlyPheCysTyrLysProPhe 17
Db 160 GATTGTCCTCTGGTGGTCTCTATGATCAGCATTCGACAGGTCCTTC 210

```

RESULT 6

```

US-09-929-230-3
; Sequence 3, Application US/09929230
; Patent No. US20020161203A1
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Bishop, Paul D.
; TITLE OF INVENTION: RATTLESNAKE VENOM GLAND PROTEINS
; FILE REFERENCE: 00-72
; CURRENT APPLICATION NUMBER: US/09/929,230
; CURRENT FILING DATE: 2001-08-13
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 453
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: This degenerate nucleotide sequence encodes the
; OTHER INFORMATION: amino acid sequence of SEQ ID NO:2.
; NAME/KEY: misc feature
; LOCATION: 9, 12, 18, 21, 24, 27, 30, 36, 39, 42, 45, 48, 51, 54, 57,
; LOCATION: 66, 69, 78, 81, 105, 111, 117, 123, 135, 141, 153, 162,
; LOCATION: 168, 171, 174, 177, 180, 189, 192, 204, 210, 213, 219, 222,
; LOCATION: 225, 231, 234, 243, 246, 258, 261, 270, 297, 306, 312, 324
; OTHER INFORMATION: n = A,T,C or G
; NAME/KEY: misc feature
; LOCATION: 330, 333, 336, 339, 348, 351, 357, 360, 366, 372, 390, 393,
; LOCATION: 405, 408, 411, 417, 432, 435, 438, 441, 447, 450, 453
; OTHER INFORMATION: n = A,T,C or G
US-09-929-230-3
Alignment Scores:
Pred. No.: 0.0368          Length: 453
Score: 66.00              Matches: 9
Percent Similarity: 64.71%  Conservative: 2
Best Local Similarity: 52.94% Mismatches: 6
Query Match: 61.11%        Indels: 0
DB: 10                    Gaps: 0

```

```

US-09-929-230-3
Alignment Scores:
Pred. No.: 0.0368          Length: 453
Score: 66.00              Matches: 9
Percent Similarity: 64.71%  Conservative: 2
Best Local Similarity: 52.94% Mismatches: 6
Query Match: 61.11%        Indels: 0
DB: 10                    Gaps: 0

```

US-09-938-114-4 (1-17) x US-09-929-230-3 (1-453)

```

QY 1 AspCysProSerGluTrpSerSerTyrGluGlyPheCysTyrLysProPhe 17
Db 58 GATGYCCNWSNGAYTGGSNWSNTAIGAYCARCAYTGTAATAAGTNTTY 108

```

RESULT 7

```

US-10-226-420-3
; Sequence 3, Application US/10226420
; Publication No. US20030157686A1
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Bishop, Paul D.
; TITLE OF INVENTION: RATTLESNAKE VENOM GLAND PROTEINS
; FILE REFERENCE: 00-72
; CURRENT APPLICATION NUMBER: US/10/226,420
; CURRENT FILING DATE: 2002-08-21
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 453
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: This degenerate nucleotide sequence encodes the
; OTHER INFORMATION: amino acid sequence of SEQ ID NO:2.
; NAME/KEY: misc feature
; LOCATION: 9, 12, 18, 21, 24, 27, 30, 36, 39, 42, 45, 48, 51, 54, 57,
; LOCATION: 66, 69, 78, 81, 105, 111, 117, 123, 135, 141, 153, 162,
; LOCATION: 168, 171, 174, 177, 180, 189, 192, 204, 210, 213, 219, 222,
; LOCATION: 225, 231, 234, 243, 246, 258, 261, 270, 297, 306, 312, 324
; OTHER INFORMATION: n = A,T,C or G
; NAME/KEY: misc feature
; LOCATION: 330, 333, 336, 339, 348, 351, 357, 360, 366, 372, 390, 393,
; LOCATION: 405, 408, 411, 417, 432, 435, 438, 441, 447, 450, 453
; OTHER INFORMATION: n = A,T,C or G
US-10-226-420-3

```

Alignment Scores:

```

Pred. No.: 0.0368          Length: 453
Score: 66.00              Matches: 9
Percent Similarity: 64.71%  Conservative: 2
Best Local Similarity: 52.94% Mismatches: 6
Query Match: 61.11%        Indels: 0
DB: 13                    Gaps: 0

```

US-09-938-114-4 (1-17) x US-10-226-420-3 (1-453)

```

QY 1 AspCysProSerGluTrpSerSerTyrGluGlyPheCysTyrLysProPhe 17
Db 58 GATGYCCNWSNGAYTGGSNWSNTAIGAYCARCAYTGTAATAAGTNTTY 108

```

RESULT 8

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US-09-929-230-7
; Sequence 7, Application US/09929230
; Patent No. US20020161203A1
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Bishop, Paul D.
; TITLE OF INVENTION: RATTLESNAKE VENOM GLAND PROTEINS
; FILE REFERENCE: 00-72
; CURRENT APPLICATION NUMBER: US/09/929,230
; CURRENT FILING DATE: 2001-08-13
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 580
; TYPE: DNA
; ORGANISM: Sistrurus miliarius
; FEATURE:

```

```
; NAME/KEY: CDS
; LOCATION: (3)...(434)
; NAME/KEY: misc_feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: Zsnk4
US-09-929-230-7

Alignment Scores:
Pred. No.: 0.0491 Length: 580
Score: 66.00 Matches: 8
Percent Similarity: 86.67% Conservative: 5
Best Local Similarity: 53.33% Mismatches: 2
Query Match: 61.11% Indels: 0
DB: 10 Gaps: 0

US-09-938-114-4 (1-17) x US-09-929-230-7 (1-580)
QY 1 AspCysProSerGluTrpSerSerTyrGluGlyPheCysTyrLys 15
Db 36 GATTGTCCTCTGATTGGTATGCGTATGATCAGTATTGCTACAGG 80

RESULT 9
US-10-226-420-7
; Sequence 94, Application US/10226420
; Publication No. US20030157686A1
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Bishop, Paul D.
; TITLE OF INVENTION: RATTLESNAKE VENOM GLAND PROTEINS
; FILE REFERENCE: 00-72
; CURRENT APPLICATION NUMBER: US/10/226,420
; CURRENT FILING DATE: 2002-08-21
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 580
; TYPE: DNA
; ORGANISM: Sistrurus miliarius
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (3)...(434)
; NAME/KEY: misc_feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: Zsnk4
US-10-226-420-7

Alignment Scores:
Pred. No.: 0.0491 Length: 580
Score: 66.00 Matches: 8
Percent Similarity: 86.67% Conservative: 5
Best Local Similarity: 53.33% Mismatches: 2
Query Match: 61.11% Indels: 0
DB: 13 Gaps: 0

US-09-938-114-4 (1-17) x US-10-226-420-7 (1-580)
QY 1 AspCysProSerGluTrpSerSerTyrGluGlyPheCysTyrLys 15
Db 36 GATTGTCCTCTGATTGGTATGCGTATGATCAGTATTGCTACAGG 80

RESULT 10
US-09-870-759-94
; Sequence 94, Application US/09870759
; Patent No. US20020177551A1
; GENERAL INFORMATION:
; APPLICANT: TERMAN, David S
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
; FILE REFERENCE: 870759
; CURRENT APPLICATION NUMBER: US/09/870,759
; CURRENT FILING DATE: 2002-01-14
; PRIOR APPLICATION NUMBER: US 60/208,128
; PRIOR FILING DATE: 2000-05-30
```

```
; NUMBER OF SEQ ID NOS: 166
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 94
; LENGTH: 5185
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (104)...(4474)
; OTHER INFORMATION:
US-09-870-759-94

Alignment Scores:
Pred. No.: 4.59 Length: 5185
Score: 61.00 Matches: 9
Percent Similarity: 71.43% Conservative: 1
Best Local Similarity: 64.29% Mismatches: 4
Query Match: 56.48% Indels: 0
DB: 10 Gaps: 0

US-09-938-114-4 (1-17) x US-09-870-759-94 (1-5185)
QY 2 CysProSerGluTrpSerSerTyrGluGlyPheCysTyrLys 15
Db 1187 TGTCTAGTCAGTGGTGGCGGTATGCGGTCACTGTTACAAG 1228

RESULT 11
US-09-751-708A-94
; Sequence 94, Application US/09751708A
; Publication No. US20030157113A1
; GENERAL INFORMATION:
; APPLICANT: TERMAN, David S
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
; FILE REFERENCE: 751708
; CURRENT APPLICATION NUMBER: US/09/751,708A
; CURRENT FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: US 60/173,371
; PRIOR FILING DATE: 1999-12-28
; NUMBER OF SEQ ID NOS: 166
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 94
; LENGTH: 5185
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (104)...(4474)
; OTHER INFORMATION:
US-09-751-708A-94

Alignment Scores:
Pred. No.: 4.59 Length: 5185
Score: 61.00 Matches: 9
Percent Similarity: 71.43% Conservative: 1
Best Local Similarity: 64.29% Mismatches: 4
Query Match: 56.48% Indels: 0
DB: 13 Gaps: 0

US-09-938-114-4 (1-17) x US-09-751-708A-94 (1-5185)
QY 2 CysProSerGluTrpSerSerTyrGluGlyPheCysTyrLys 15
Db 1187 TGTCTAGTCAGTGGTGGCGGTATGCGGTCACTGTTACAAG 1228

RESULT 12
US-09-929-230-9
; Sequence 9, Application US/09929230
; Patent No. US20020161203A1
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Bishop, Paul D.
; TITLE OF INVENTION: RATTLESNAKE VENOM GLAND PROTEINS
; FILE REFERENCE: 00-72
```

;; CURRENT APPLICATION NUMBER: US/09/929,230
;; NUMBER OF SEQ ID NOS: 14
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 9
;; LENGTH: 432
;; TYPE: DNA
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: This degenerate nucleotide sequence encodes the
;; OTHER INFORMATION: amino acid sequence of SEQ ID NO:8.
;; NAME/KEY: misc feature
;; LOCATION: 6, 15, 18, 21, 24, 27, 42, 45, 57, 78, 81, 93, 96, 99, 111,
;; LOCATION: 117, 126, 135, 141, 144, 150, 153, 156, 165, 171, 177, 180,
;; LOCATION: 186, 189, 195, 198, 201, 231, 240, 243, 246, 255, 273, 276,
;; LOCATION: 285, 291, 294, 297, 300, 315, 327, 330, 345, 348, 360
;; OTHER INFORMATION: n = A,T,C or G
;; NAME/KEY: misc feature
;; LOCATION: 363, 369, 372, 378, 384, 393, 405, 423, 426
;; OTHER INFORMATION: n = A,T,C or G
US-09-929-230-9

Alignment Scores:
Pred. No.: 0.374 Length: 432
Score: 60.00 Matches: 7
Percent Similarity: 78.57% Conservative: 4
Best Local Similarity: 50.00% Mismatches: 3
Query Match: 55.56% Indels: 0
DB: 10 Gaps: 0

US-09-938-114-4 (1-17) x US-09-929-230-9 (1-432)
QY 1 AspCysProSerGluTrpSerSerTyrrGluGlyPheCysTyr 14
Db 34 GAYTGYCCNWSNGAYTGGTAYGCNTAYGAYCARTAYTGYTAY 75

RESULT 13
US-10-226-420-9
; Sequence 9, Application US/10226420
; Publication No. US20030157686A1
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Bishop, Paul D.
; TITLE OF INVENTION: RATTLESNAKE VENOM GLAND PROTEINS
; FILE REFERENCE: 00-72
; CURRENT APPLICATION NUMBER: US/10/226,420
; CURRENT FILING DATE: 2002-08-21
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 432
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: This degenerate nucleotide sequence encodes the
; OTHER INFORMATION: amino acid sequence of SEQ ID NO:8.
; NAME/KEY: misc feature
; LOCATION: 6, 15, 18, 21, 24, 27, 42, 45, 57, 78, 81, 93, 96, 99, 111,
; LOCATION: 117, 126, 135, 141, 144, 150, 153, 156, 165, 171, 177, 180,
; LOCATION: 186, 189, 195, 198, 201, 231, 240, 243, 246, 255, 273, 276,
; LOCATION: 285, 291, 294, 297, 300, 315, 327, 330, 345, 348, 360
; OTHER INFORMATION: n = A,T,C or G
; NAME/KEY: misc feature
; LOCATION: 363, 369, 372, 378, 384, 393, 405, 423, 426
; OTHER INFORMATION: n = A,T,C or G
US-10-226-420-9

Alignment Scores:
Pred. No.: 0.374 Length: 432
Score: 60.00 Matches: 7
Percent Similarity: 78.57% Conservative: 4

Best Local Similarity: 50.00% Mismatches: 3
Query Match: 55.56% Indels: 0
DB: 13 Gaps: 0
US-09-938-114-4 (1-17) x US-10-226-420-9 (1-432)
QY 1 AspCysProSerGluTrpSerSerTyrrGluGlyPheCysTyr 14
Db 34 GAYTGYCCNWSNGAYTGGTAYGCNTAYGAYCARTAYTGYTAY 75

RESULT 14
US-09-764-870-37
; Sequence 37, Application US/09764870
; Patent No. US20020042386A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PTZ14
; CURRENT APPLICATION NUMBER: US/09/764,870
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 646
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 37
; LENGTH: 618
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (48)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (65)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (556)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (588)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (598)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-764-870-37

Alignment Scores:
Pred. No.: 1.26 Length: 618
Score: 58.00 Matches: 8
Percent Similarity: 76.92% Conservative: 2
Best Local Similarity: 61.54% Mismatches: 3
Query Match: 53.70% Indels: 0
DB: 9 Gaps: 0

US-09-938-114-4 (1-17) x US-09-764-870-37 (1-618)
QY 2 CysProSerGluTrpSerSerTyrrGluGlyPheCysTyr 14
Db 247 TGCCCCACGTGGTGGTCTTCCTCGAGGGGCTCTGCTAC 285

RESULT 15
US-10-125-540-37
; Sequence 37, Application US/10125540
; Publication No. US20030059875A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PTZ14C1
; CURRENT APPLICATION NUMBER: US/10/125,540
; CURRENT FILING DATE: 2002-04-19
; Prior application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 646
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 37

Tue Dec 9 09:26:59 2003

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; LENGTH: 618
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (48)
; OTHER INFORMATION: n equals a,t,g, or c
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (65)
; OTHER INFORMATION: n equals a,t,g, or c
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (556)
; OTHER INFORMATION: n equals a,t,g, or c
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (588)
; OTHER INFORMATION: n equals a,t,g, or c
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (598)
; OTHER INFORMATION: n equals a,t,g, or c
US-10-125-540-37

```

```

Alignment Scores:
Pred. No.: 1.26 Length: 618
Score: 58.00 Matches: 8
Percent Similarity: 76.92% Conservative: 2
Best Local Similarity: 61.54% Mismatches: 3
Query Match: 53.70% Indels: 0
DB: 15 Gaps: 0

```

US-09-938-114-4 (1-17) x US-10-125-540-37 (1-618)

```

Qy      2 CysProSerGluTrpSerSerTyrGluGlyPheCysTyr 14
         |||||:::|||||
Db      247 TGCCCCACGTCGTGGCTGCTTCGAGGGCTCCTGCTAC 285

```

Search completed: December 8, 2003, 19:36:07
Job time : 69.6114 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 8, 2003, 09:49:54 ; Search time 3.4 Seconds
(without alignments)
480.843 Million cell updates/sec

Title: US-09-938-114-4

Perfect score: 108

Sequence: 1 DCPSEWSYEGFCYKPF 17

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 76:*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	101	93.5	146	2 JC71135	agkisacutacin beta
2	98	90.7	146	2 JC4691	coagulation factor
3	94	87.0	129	2 JC4329	coagulation factor
4	94	87.0	146	2 JC7105	aggregin beta chain
5	84	77.8	30	2 B53088	factor IX/factor X
6	82	75.9	40	2 S56006	tokaracetin alpha
7	81	75.0	30	2 A53088	factor IX/factor X
8	81	75.0	133	2 A47267	botrocetin alpha c
9	79	73.1	125	2 B47267	botrocetin beta ch
10	77	71.3	40	2 A56829	alboaggregin-B bet
11	77	71.3	152	2 JC71134	agkisacutacin alph
12	76	70.4	152	2 JC4690	coagulation factor
13	75	69.4	40	2 S56007	tokaracetin beta c
14	71	65.7	123	2 B42972	coagulation factor
15	69	63.9	40	2 B56829	alboaggregin-B alp
16	67	62.0	123	2 JC2415	echicetin beta cha
17	64	59.3	125	2 JC5059	bitiscetin beta ch
18	64	59.3	131	2 JC5058	bitiscetin alpha c
19	62	57.4	29	2 PC4421	multicatalase (EC 3
20	61	56.5	1456	1 A36563	mannose receptor p
21	58	53.7	16	2 A48630	bothrojaracin - ja
22	58	53.7	71	2 S55679	flavocetin A - hab
23	55	50.9	284	1 LNRTL	hepatic lectin - x
24	55	50.9	284	2 S29855	asialoglycoprotein
25	55	50.9	1455	1 A48925	mannose receptor p
26	54	50.0	46	2 FX0080	lectin SPL-2, Ca2+
27	54	50.0	135	2 A38609	lectin, galactose-
28	54	50.0	2415	1 A39086	aggreacan precursor
29	53	49.1	143	2 D71009	hypothetical prote

ALIGNMENTS

RESULT 1

JC71135

agkisacutacin beta chain precursor - sharp-nosed viper

N/Alternate names: fibrinogenolytic venom protein

C/Species: Agkistrodon acutus (sharp-nosed viper)

C/Date: 04-Mar-2000 #sequence_revision 04-Mar-2000 #text_change 24-Oct-2000

C/Accession: JC71135; PC7038

R/Cheng, X.; Qian, Y.; Liu, Q.; Li, B.X.Y.; Zhang, M.; Liu, J.

Biochem. Biophys. Res. Commun. 265, 530-535, 1999

A/Title: Purification, characterization, and cDNA cloning of a new fibrinogenolytic venom

A/Reference number: JC71134; MUID:20025379; PMID:10558903

A/Accession: JC71135

A/Molecule type: mRNA

A/Residues: 1-146 <CH2>

A/Cross-references: GB:AF176421

A/Experimental source: venom gland

A/Accession: PC7038

A/Molecule type: protein

A/Residues: 24-50;59-83;102-107;112-114 <CH2>

C/Superfamily: tetranectin; C-type lectin homology

C/Keywords: disulfide bond; heterodimer; venom

F/1-23/Domain: signal sequence #status predicted <SIG>

F/24-146/Product: agkisacutacin beta chain #status experimental <MAT>

Query Match

Best Local Similarity 93.5%; Score 101; DB 2; Length 146;

Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DCPSEWSYEGFCYKPF 17

Db 24 DCPSEWSYEGHCYKPF 40

RESULT 2

JC4691

coagulation factor IX/factor X-binding protein chain A precursor - habu

C/Species: Trimeresurus flavoviridis (habu)

C/Date: 16-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 20-Jun-2000

C/Accession: JC4691; B39332; JC4330

R/Matsuzaki, R.; Yoshiara, E.; Yamada, M.; Shima, K.; Atoda, H.; Morita, T.

Biochem. Biophys. Res. Commun. 220, 382-387, 1996

A/Title: cDNA cloning of IX/X-BP, a heterogeneous two-chain anticoagulant protein from sr

A/Reference number: JC4690; MUID:96184662; PMID:8645314

A/Accession: JC4691

A/Molecule type: mRNA

A/Residues: 1-146 <MAT1>

A/Cross-references: DDBJ:D83332; NID:gl402641; PIDN:BAA11888.1; PID:gl402642

A/Experimental source: venom

R/Atoda, H.; Hyuga, M.; Morita, T.

J. Biol. Chem. 266, 14903-14911, 1991

A/Title: The primary structure of coagulation factor IX/factor X-binding protein isolates: otein, tetranectin, and lymphocyte Fc epsilon receptor for immunoglobulin E.

```

Best Local Similarity 88.2%; Pred.No. 3.9e-06;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 DCPSEWSSYEGFCYKPF 17
    ||||| ||||| |||||
Db 24 DCPSGWSSYEGHCYKPF 40

RESULT 5
B53088
factor IX/factor X-binding anticoagulant protein A chain - jararaca (fragment)
C;Species: Bothrops jararaca (jararaca)
C;Date: 13-Sep-1994 #sequence_revision 18-Nov-1994 #text_change 15-Jun-1996
C;Accession: B53088
R;Sekiya, F.; Atoda, H.; Morita, T.
Biochemistry 32, 6892-6897, 1993
A;Title: Isolation and characterization of an anticoagulant protein homologous
A;Reference number: A53088; MUID:93326575; PMID:8334120
A;Accession: B53088
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-30 <SEK>
A;Experimental source: venom
A;Note: sequence extracted from NCBI backbone (NCBIP:135336)

Query Match 77.8%; Score 84; DB 2; Length 30;
Best Local Similarity 76.5%; Pred.No. 2.7e-05;
Matches 13; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 DCPSEWSSYEGFCYKPF 17
    ||||| ||||| |||||
Db 1 DCPSDWSPYEGHCYKHF 17

RESULT 6
S56006
tokaracatin alpha chain - Trimeresurus tokarensis (fragment)
N;Alternate names: platelet aggregation inhibitor; platelet antagonist
C;Species: Trimeresurus tokarensis
C;Date: 10-Oct-1995 #sequence_revision 08-Nov-1996 #text_change 07-May-1999
C;Accession: S56006
R;Kawasaki, T.; Tanuchi, Y.; Hisamichi, N.; Fujimura, Y.; Suzuki, M.; Titani,
Biochem. J. 308, 947-953, 1995
A;Title: Tokaracatin, a new platelet antagonist that binds to platelet glycoprotein
A;Reference number: S56006; MUID:97104297; PMID:8948455
A;Accession: S56006
A;Molecule type: protein
A;Residues: 1-40 <KAW>
C;Superfamily: tetranectin; C-type lectin homology

Query Match 75.9%; Score 82; DB 2; Length 40;
Best Local Similarity 70.6%; Pred.No. 6.5e-05;
Matches 12; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 DCPSEWSSYEGFCYKPF 17
    ||||| ||||| |||||
Db 1 DCPSGWSSYEGHCYKPF 17

RESULT 7
A53088
factor IX/factor X-binding anticoagulant protein B chain - jararaca (fragment)
C;Species: Bothrops jararaca (jararaca)
C;Date: 13-Sep-1994 #sequence_revision 18-Nov-1994 #text_change 15-Jun-1996
C;Accession: A53088
R;Sekiya, F.; Atoda, H.; Morita, T.
Biochemistry 32, 6892-6897, 1993
A;Title: Isolation and characterization of an anticoagulant protein homologous
A;Reference number: A53088; MUID:93326575; PMID:8334120
A;Accession: A53088
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-30 <SEK>

```

A;Experimental source: venom

A;Note: sequence extracted from NCBI backbone (NCBIP:135337)

Query Match 75.0%; Score 81; DB 2; Length 30;
Best Local Similarity 70.6%; Pred. No. 7e-05;
Matches 12; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 DCPSEWSSYEGFCYKPF 17
|||:|||||:|
Db 1 DCPSDWSPYEGHCYRVF 17

RESULT 8

A47267
botroctetin alpha chain - jararaca
N;Alternate names: two chain botrocetin alpha chain
C;Species: Bothrops jararaca (jararaca)
C;Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 15-May-1998
C;Accession: A47267; B37958
R;Usami, Y.; Fujimura, Y.; Suzuki, M.; Ozeki, Y.; Nishio, K.; Fukui, H.; Titani, K.
Proc. Natl. Acad. Sci. U.S.A. 90, 928-932, 1993
A;Title: Primary structure of two-chain botrocetin, a von Willebrand factor modulator protein
A;Reference number: A47267; MUID:93157385; PMID:8430107
A;Accession: A47267
A;Molecule type: protein
A;Residues: 1-133 <USA>
A;Experimental source: venom
A;Note: sequence extracted from NCBI backbone (NCBIP:124085)
R;Fujimura, Y.; Titani, K.; Usami, Y.; Suzuki, M.; Oyama, R.; Matsui, T.; Fukui, H.; Sug
Biochemistry 30, 1957-1964, 1991
A;Title: Isolation and chemical characterization of two structurally and functionally di
A;Reference number: A37958; MUID:91129280; PMID:1993206
A;Accession: B37958
A;Molecule type: protein
A;Residues: 1-40 <FUJ>

C;Complex: heterodimer of alpha and beta (see PIR:B47267) chains
C;Superfamily: tetranectin; C-type lectin homology
C;Keywords: hemagglutinin; heterodimer; venom
F;2-128/Domain: C-type lectin homology <LCH>
F;2-13,30-128,103-120/Disulfide bonds: #status experimental
F;80/Disulfide bonds: interchain (to beta-75) #status experimental

Query Match 75.0%; Score 81; DB 2; Length 133;
Best Local Similarity 82.4%; Pred. No. 0.00024;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 DCPSEWSSYEGFCYKPF 17
|||:|||||:|
Db 1 DCPSGWSSYEGHCYKPF 17

RESULT 9

B47267
botroctetin beta chain - jararaca
N;Alternate names: two chain botrocetin beta chain
C;Species: Bothrops jararaca (jararaca)
C;Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 15-May-1998
C;Accession: B47267; C37958
R;Usami, Y.; Fujimura, Y.; Suzuki, M.; Ozeki, Y.; Nishio, K.; Fukui, H.; Titani, K.
Proc. Natl. Acad. Sci. U.S.A. 90, 928-932, 1993
A;Title: Primary structure of two-chain botrocetin, a von Willebrand factor modulator pr
A;Reference number: A47267; MUID:93157385; PMID:8430107
A;Accession: B47267
A;Molecule type: protein
A;Residues: 1-125 <USA>
A;Experimental source: venom
A;Note: sequence extracted from NCBI backbone (NCBIP:124086)
R;Fujimura, Y.; Titani, K.; Usami, Y.; Suzuki, M.; Oyama, R.; Matsui, T.; Fukui, H.; Sug
Biochemistry 30, 1957-1964, 1991
A;Title: Isolation and chemical characterization of two structurally and functionally di
A;Reference number: A37958; MUID:91129280; PMID:1993206
A;Accession: C37958
A;Molecule type: protein

A;Residues: 1-40 <FUJ>

C;Complex: heterodimer of alpha (see PIR:A47267) and beta chains
C;Superfamily: tetranectin; C-type lectin homology
C;Keywords: hemagglutinin; heterodimer; venom

F;2-121/Domain: C-type lectin homology <LCH>
F;2-13,30-121,98-113/Disulfide bonds: #status experimental
F;75/Disulfide bonds: interchain (to alpha-80) #status experimental

Query Match 73.1%; Score 79; DB 2; Length 125;
Best Local Similarity 70.6%; Pred. No. 0.00043;
Matches 12; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 DCPSEWSSYEGFCYKPF 17
|||:|||||:|
Db 1 DCPDWSYEGHCYRVF 17

RESULT 10

A56829
alboaggregin-B beta chain - green pit viper (fragment)
C;Species: Trimeresurus albolabris (green pit viper)
C;Date: 05-Jan-1996 #sequence_revision 05-Jan-1996 #text_change 05-Jan-1996
C;Accession: A56829
R;Yoshida, E.; Fujimura, Y.; Miura, S.; Sugimoto, M.; Fukui, H.; Narita, N.; Usami, Y.; S
Biochem. Biophys. Res. Commun. 191, 1386-1392, 1993
A;Title: Alboaggregin-B and botrocetin, two snake venom proteins with highly homologous a
A;Reference number: A56829; MUID:93221514; PMID:8466514
A;Accession: A56829
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-40 <YOS>
A;Experimental source: venom
A;Note: sequence extracted from NCBI backbone (NCBIP:128750)
C;Keywords: disulfide bond; heterodimer

Query Match 71.3%; Score 77; DB 2; Length 40;
Best Local Similarity 64.7%; Pred. No. 0.00032;
Matches 11; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 DCPSEWSSYEGFCYKPF 17
|||:|||||:|
Db 1 DCPDWSYDYLCYRVF 17

RESULT 11

JC7134
agkisacutacin alpha chain precursor - sharp-nosed viper
N;Alternate names: fibrinogenolytic venom protein
C;Species: Agkistrodon acutus (sharp-nosed viper)
C;Date: 04-Mar-2000 #sequence_revision 04-Mar-2000 #text_change 24-Oct-2000
C;Accession: JC7134; PC7037
R;Cheng, X.; Qian, Y.; Liu, Q.; Li, B.X.Y.; Zhang, M.; Liu, J.
Biochem. Biophys. Res. Commun. 265, 530-535, 1999
A;Title: Purification, characterization, and cDNA cloning of a new fibrinogenolytic venom
A;Reference number: JC7134; MUID:20025379; PMID:10558903
A;Accession: JC7134
A;Molecule type: mRNA
A;Residues: 1-152 <CHE>
A;Cross-references: GB:AF176420
A;Experimental source: venom gland
A;Accession: PC7037
A;Molecule type: protein
A;Residues: 24-53;84-86;87-94;125-136;137-152 <CH2>
C;Superfamily: tetranectin; C-type lectin homology
C;Keywords: disulfide bond; heterodimer; venom
F;1-23/Domain: signal sequence #status predicted <SIG>
F;24-152/Product: agkisacutacin alpha chain #status experimental <MAT>

Query Match 71.3%; Score 77; DB 2; Length 152;
Best Local Similarity 76.5%; Pred. No. 0.00097;
Matches 13; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 DCPSEWSSYEGFCYKPF 17

Db 24 DCSSGWSYEGHCYKVF 40
|| | ||||| ||| |

RESULT 12

JC4690
coagulation factor IX/factor X-binding protein chain A precursor - habu
C;Species: Trimeresurus flavoviridis (habu)
C;Date: 16-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 20-Jun-2000
C;Accession: JC4690; A39332
R;Matsuzaki, R.; Yoshiara, E.; Yamada, M.; Shima, K.; Atoda, H.; Morita, T.
Biochem. Biophys. Res. Commun. 220, 382-387, 1996
A;Title: cDNA cloning of IX/X-BP, a heterogeneous two-chain anticoagulant protein from s
A;Reference number: JC4690; MUID:96184662; PMID:8645314
A;Accession: JC4690
A;Molecule type: mRNA
A;Residues: 1-152 <MAT1>
A;Cross-references: DDBJ:D83331; NID:gl402639; PIDN:BAAl1887.1; PID:gl402640
A;Experimental source: venom
R;Atoda, H.; Hyuga, M.; Morita, T.
J. Biol. Chem. 266, 14903-14911, 1991
A;Title: The primary structure of coagulation factor IX/factor X-binding protein isolate
otein, tetranectin, and lymphocyte Fc epsilon receptor for immunoglobulin E.
A;Reference number: A39332; MUID:91332000; PMID:1831197
A;Accession: A39332
A;Status: preliminary
A;Molecule type: protein
C;Superfamily: tetranectin; C-type lectin homology
C;Keywords: anticoagulant; blood coagulation; glycoprotein; hemolymph; lectin
F;1-23/Domain: signal sequence #status predicted <SIG>
F;24-152/Product: factor IX/X binding protein chain A #status predicted <MAT>
F;25-150/Domain: C-type lectin homology <LCH>
F;25-36,53-150,125-142/Disulfide bonds: #status predicted

Query Match 70.4%; Score 76; DB 2; Length 152;
Best Local Similarity 76.5%; Pred. No. 0.0013;
Matches 13; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 DCPSEWSSYEGFCYKPF 17
|| | ||||| ||| |
Db 24 DCUSGWSYEGHCYKVF 40

RESULT 13

S56007
tokaracetin beta chain - Trimeresurus tokarensis (fragment)
N;Alternate names: platelet aggregation inhibitor; platelet antagonist
C;Species: Trimeresurus tokarensis
C;Date: 10-Oct-1995 #sequence_revision 08-Nov-1996 #text_change 07-May-1999
C;Accession: S56007
R;Kawasaki, T.; Taniuchi, Y.; Hisamichi, N.; Fujimura, Y.; Suzuki, M.; Titani, K.; Sakai
Biochem. J. 308, 947-953, 1995
A;Title: Tokaracetin, a new platelet antagonist that binds to platelet glycoprotein Ib a
A;Reference number: S56006; MUID:97104297; PMID:8948455
A;Accession: S56007
A;Molecule type: protein
A;Residues: 1-40 <KAW>

Query Match 69.4%; Score 75; DB 2; Length 40;
Best Local Similarity 64.7%; Pred. No. 0.0062;
Matches 11; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 1 DCPSEWSSYEGFCYKPF 17
|| | ||||| ||| |
Db 1 DCPDWSYDEHCYRVF 17

RESULT 14

B42972
coagulation factor X activating enzyme (EC 3.4.24.-) light chain - Russell's viper
C;Species: Vipera russelli (Russell's viper)
C;Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 28-Feb-1997

C;Accession: B42972
R;Takeya, H.; Nishida, S.; Miyata, T.; Kawada, S.; Saisaka, Y.; Morita, T.; Iwanaga, S.
J. Biol. Chem. 267, 14109-14117, 1992
A;Title: Coagulation factor X activating enzyme from Russell's viper venom (RVV-X). A no
A;Reference number: A42972; MUID:92332516; PMID:1629211
A;Contents: V. r. siamensis
A;Accession: B42972
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-123 <TAK>
A;Experimental source: venom
A;Superfamily: tetranectin; C-type lectin homology
C;Keywords: hydrolase; metalloproteinase; venom; zinc
F;4-121/Domain: C-type lectin homology <LCH>
F;4-121,32-121,98-113/Disulfide bonds: #status predicted

Query Match 65.7%; Score 71; DB 2; Length 123;
Best Local Similarity 70.6%; Pred. No. 0.0056;
Matches 12; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 DCPSEWSSYEGFCYKPF 17
|| | ||||| ||| |
Db 3 DCPSGWLSYEGHCYKGF 19

RESULT 15

B56829
alboaggregin-B alpha chain - green pit viper (fragment)
C;Species: Trimeresurus albolabris (green pit viper)
C;Date: 05-Jan-1996 #sequence_revision 05-Jan-1996 #text_change 03-May-1996
C;Accession: B56829
R;Yoshida, E.; Fujimura, Y.; Miura, S.; Sugimoto, M.; Fukui, H.; Narita, N.; Usami, Y.;
Biochem. Biophys. Res. Commun. 191, 1386-1392, 1993
A;Title: Alboaggregin-B and botrocetin, two snake venom proteins with highly homologous
A;Reference number: A56829; MUID:93221514; PMID:8466514
A;Accession: B56829
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-40 <YOS>
A;Experimental source: venom
A;Note: sequence extracted from NCBI backbone (NCBIP:128751)
C;Superfamily: tetranectin; C-type lectin homology
C;Keywords: disulfide bond; heterodimer

Query Match 63.9%; Score 69; DB 2; Length 40;
Best Local Similarity 60.0%; Pred. No. 0.0042;
Matches 9; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DCPSEWSSYEGFCYK 15
|| | ||||| ||| |
Db 1 DCFSDWSSFKQYCYQ 15

Search completed: December 8, 2003, 09:55:35
Job time : 3.4 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 8, 2003, 09:46:14 ; Search time 2.23429 Seconds
(without alignments)
357.812 Million cell updates/sec

Title: US-09-938-114-4
Perfect score: 108
Sequence: 1 DCPSEWSYEGFCYKPF 17

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	98	90.7	146	1	IXB_TRIFL
2	86	79.6	117	1	CHBB_CROHO
3	86	79.6	123	1	ABA4_TRIAB
4	83	76.9	127	1	CHBA_CROHO
5	81	75.0	133	1	BOTA_BOTJA
6	80	74.1	118	1	ABBB_TRIAB
7	80	74.1	125	1	ABAB_TRIAB
8	79	73.1	131	1	BOTB_BOTJA
9	79	73.1	131	1	ABAL_TRIAB
10	76	70.4	152	1	IXA_TRIFL
11	74	68.5	148	1	CVXB_CRODU
12	72	66.7	133	1	RHCA_AGRKH
13	69	63.9	132	1	ABBA_TRIAB
14	67	62.0	123	1	ECHE_ECHCA
15	64	59.3	129	1	RHCB_AGRKH
16	64	59.3	133	1	ECHE_ECHCA
17	62	57.4	29	1	MULR_ECHML
18	61	56.5	1456	1	MANR_HUMAN
19	56	51.9	158	1	CVXA_CRODU
20	55	50.9	283	1	LECH_MOUSE
21	55	50.9	283	1	LECH_RAT
22	54	50.0	135	1	LECG_CROAT
23	54	50.0	2415	1	PGCA_HUMAN
24	53	49.1	304	1	MMGL_MOUSE
25	52	48.1	158	1	KGFE_HUMAN
26	52	48.1	158	1	KGFE_PANTR
27	52	48.1	231	1	KGFC_HUMAN
28	52	48.1	231	1	KGCC_HUMAN
29	52	48.1	233	1	KGCA_HUMAN
30	52	48.1	233	1	KGGA_HUMAN
31	52	48.1	233	1	KGGA_PANTR
32	52	48.1	240	1	KGGE_HUMAN
33	52	48.1	240	1	KGGE_PANTR

34	51	47.2	134	1	ABA2_TRIAB
35	51	47.2	168	1	VA40_VACCC
36	51	47.2	168	1	VA40_VACCV
37	51	47.2	306	1	MMGL_RAT
38	51	47.2	548	1	IDD_MOUSE
39	51	47.2	883	1	PGCB_MOUSE
40	51	47.2	912	1	PGCB_BOVIN
41	50	46.3	167	1	V008_FOWPV
42	50	46.3	2124	1	PGCA_RAT
43	50	46.3	2132	1	PGCA_MOUSE
44	50	46.3	2364	1	PGCA_BOVIN
45	49	45.4	175	1	ANP_OSMMO

ALIGNMENTS

RESULT 1
IXB_TRIFL
ID - IXB TRIFL STANDARD; PRT; 146 AA.
AC P23807; Q91247;
DT 01-NOV-1991 (Rel. 20, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Coagulation factor IX/factor X-binding protein B chain precursor (IX/X-BP).
DE Trimeresurus flavoviridis (Habu).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidodactylia; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Crotalinae; Trimeresurus.
OX NCBI_TaxID=88087;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96184662; PubMed=8645314;
RA Matsuzaki R., Yoshihara E., Yamada M., Shima K., Atoda H., Morita T.;
RT "CDNA cloning of IX/X-BP, a heterogeneous two-chain anticoagulant protein from snake venom.";
RL Biochem. Biophys. Res. Commun. 220:382-387 (1996).
RN [2]
RP SEQUENCE OF 24-146.
RC TISSUE=Venom;
RX MEDLINE=91332000; PubMed=1831197;
RA Atoda H., Hyuga M., Morita T.;
RT "The primary structure of coagulation factor IX/factor X-binding protein isolated from the venom of Trimeresurus flavoviridis. Homology with asialoglycoprotein receptors, proteoglycan core protein, tetranectin, and lymphocyte Fc epsilon receptor for immunoglobulin E.";
RL J. Biol. Chem. 266:14903-14911 (1991).
RN [3]
RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).
RX MEDLINE=97331317; PubMed=9187649;
RA Mizuno H., Fujimoto Z., Koizumi M., Kano H., Atoda H., Morita T.;
RT "Structure of coagulation factors IX/X-binding protein, a heterodimer of C-type lectin domains.";
RL Nat. Struct. Biol. 4:438-441 (1997).
CC -|- FUNCTION: ANTICOAGULANT PROTEIN WHICH BINDS WITH FACTOR IX AND FACTOR X IN THE PRESENCE OF CALCIUM WITH A 1 TO 1 STOICHIOMETRY.
CC -|- SUBUNIT: HETERODIMER OF CHAINS A AND B LINKED BY A DISULFIDE BOND.
CC -|- SUBCELLULAR LOCATION: Secreted.
CC -|- MISCELLANEOUS: CALCIUM IS REQUIRED FOR LIGAND BINDING.
CC -|- SIMILARITY: Contains 1 C-type lectin family domain.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).
DR EMBL; D83332; BAAL1888.1; -;
DR PIR; JC4691; JC4691.

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DR PDB; 1LXX; 06-MAY-98.
DR PDB; 1BJ3; 16-AUG-99.
DR InterPro; IPR001304; Lectin C.
DR Pfam; PF00059; lectin c; 1.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS00615; C-TYPE LECTIN_1; 1.
DR PROSITE; PS50041; C-TYPE LECTIN_2; 1.
KW Lectin; Calcium; Signal; 3D-structure.
FT SIGNAL 1 23
FT CHAIN 24 146
FT DOMAIN 24 144
FT DISULFID 25 36
FT DISULFID 53 142
FT DISULFID 98 98
FT DISULFID 119 134
FT TURN 27 28
FT TURN 30 32
FT TURN 33 34
FT STRAND 35 44
FT STRAND 46 54
FT HELIX 55 56
FT TURN 58 59
FT STRAND 61 62
FT HELIX 68 82
FT STRAND 86 88
FT TURN 94 97
FT STRAND 100 102
FT TURN 103 104
FT STRAND 113 113
FT STRAND 118 123
FT TURN 124 125
FT STRAND 126 133
FT TURN 134 135
FT STRAND 138 146
SQ SEQUENCE 146 AA; 16922 MW; 8E1961C59F96757C CRC64;

Query Match 90.7%; Score 98; DB 1; Length 146;
Best Local Similarity 88.2%; Pred. No. 1.8e-07;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 DCPSEWSSYEGFCYKPF 17
Db 24 DCPSDWSSYEGHCYRVF 40
|||||:|||||:|||||

RESULT 2
CHBB CROHO STANDARD; PRT; 117 AA.
AC P81509;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE CH-B beta subunit.
OS Crotales horridus horridus (Timber rattlesnake).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroides;
OC Viperidae; Crotalinae; Crotalus.
OX NCBI_TaxID=8747;
RN [1]
RP SEQUENCE.
RC TISSUE=Venom;
RX MEDLINE=96420502; PubMed=823201;
RA Andrews R.K., Kroll M.H., Ward C.M., Rose J.W., Scarborough R.M.,
RA Smith A.I., Lopez J.A., Berndt M.C.;
RT "Binding of a novel 50-kilodalton aldoaggregin from Trimeresurus
RT albobabris and related viper venom proteins to the platelet membrane
RT glycoprotein Ib-IX-v complex. Effect on platelet aggregation and
RT glycoprotein Ib-mediated platelet activation.";
RL Biochemistry 35:12629-12639(1996).
CC -1- FUNCTION: Binds to platelet GPIb/IX receptor system, inhibits VWF
CC binding, and stimulates agglutination.
CC -1- SUBUNIT: Heterodimer of alpha and beta subunits; disulfide-linked.

-1- SUBCELLULAR LOCATION: Secreted.
-1- SIMILARITY: Contains 1 C-type lectin family domain.
SMART; SM00034; CLECT; 1.
PROSITE; PS00615; C-TYPE LECTIN_1; 1.
PROSITE; PS50041; C-TYPE LECTIN_2; 1.
DOMAIN 9 116 C-TYPE LECTIN.
DISULFID 2 13 BY SIMILARITY.
DISULFID 30 115 BY SIMILARITY.
DISULFID 92 92 INTERCHAIN (WITH C-81 IN ALPHA CHAIN) (POTENTIAL).
DISULFID 95 107 BY SIMILARITY.
SEQUENCE 117 AA; 13888 MW; 07835BBBC61E9EAD CRC64;

Query Match 79.6%; Score 86; DB 1; Length 117;
Best Local Similarity 76.5%; Pred. No. 8e-06;
Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 1 DCPSEWSSYEGFCYKPF 17
Db 1 DCPSDWSSYEGHCYRVF 17
|||||:|||||:|||||

RESULT 3
ABA4 TRIAB STANDARD; PRT; 123 AA.
AC P8114;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Alboaggregin A subunit 4.
OS Trimeresurus albobabris (White-lipped pit viper).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroides;
OC Viperidae; Crotalinae; Trimeresurus.
OX NCBI_TaxID=8765;
RN [1]
RP SEQUENCE.
RC TISSUE=Venom;
RX MEDLINE=98189535; PubMed=9531050;
RA Kowalska M.A., Tan L., Holt J.C., Peng M., Karczewski J.,
RA Calvete J.J., Niewiarowski S.;
RT "Alboaggregins A and B. Structure and interaction with human
RT platelets.";
RL Thromb. Haemost. 79:609-613(1998).
CC -1- FUNCTION: Binds to platelet GPIb/IX receptor system and stimulates
CC agglutination.
CC -1- SUBUNIT: Heterotetramer of the subunits 1, 2, 3 and 4,
CC disulfide-linked.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Contains 1 C-type lectin family domain.
HSSP; P23807; 1LXX.
DR InterPro; IPR002353; AntifreezeII.
DR InterPro; IPR001304; Lectin C.
DR Pfam; PF00059; lectin c; 1.
DR PRINTS; PR00356; ANTIFREEZEII.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS00615; C-TYPE LECTIN_1; 1.
DR PROSITE; PS50041; C-TYPE LECTIN_2; 1.
KW Lectin.
FT DOMAIN 1 121 C-TYPE LECTIN (LONG FORM).
FT DISULFID 2 13 BY SIMILARITY.
FT DISULFID 30 119 BY SIMILARITY.
FT DISULFID 96 111 BY SIMILARITY.
SQ SEQUENCE 123 AA; 14365 MW; D4CFBEE1219C9B1E CRC64;

Query Match 79.6%; Score 86; DB 1; Length 123;
Best Local Similarity 76.5%; Pred. No. 8.4e-06;
Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 1 DCPSEWSSYEGFCYKPF 17
Db 1 DCPSDWSSYEGHCYRVF 17
|||||:|||||:|||||

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RESULT 4
CHBA_CROHO
ID CHBA_CROHO STANDARD; PRT; 127 AA.
AC P81508;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE CHB-B alpha subunit.
OS Crotales horridus horridus (Timber rattlesnake).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Crotalinae; Crotalus.
OX NCBI_TaxID=8747;
RN [1]
RP SEQUENCE.
RC TISSUE=Venom;
RX MEDLINE=96420502; PubMed=8823201;
RA Andrews R.K., Kroll M.H., Ward C.M., Rose J.W., Scarborough R.M.,
RA Smith A.I., Lopez J.A., Bernd M.C.;
RT "Binding of a novel 50-kilodalton albosaggregin from Trimeresurus
RT albolabris and related viper venom proteins to the platelet membrane
RT glycoprotein Ib-IX-V complex. Effect on platelet aggregation and
RT glycoprotein Ib-mediated platelet activation.";
RL Biochemistry 35:12629-12639(1996).
CC -1- FUNCTION: Binds to platelet GPIb/IX receptor system, inhibits VWF
CC -1- binding, and stimulates agglutination.
CC -1- SUBUNIT: Heterodimer of alpha and beta subunits; disulfide-linked.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Contains 1 C-type lectin family domain.
DR SMART, SM00034; CLECT; 1.
DR PROSITE, PS00645; C_TYPE_LLECTIN_1; FALSE_NEG.
DR PROSITE, PS00041; C_TYPE_LLECTIN_2; 1.
KW Lectin.
FT DOMAIN 11 121 C-TYPE LECTIN.
FT DISULFID 4 15 BY SIMILARITY.
FT DISULFID 32 120 BY SIMILARITY.
FT DISULFID 81 81 INTERCHAIN (WITH C-92 IN BETA CHAIN)
(POTENTIAL).
FT DISULFID 95 112 BY SIMILARITY.
SQ SEQUENCE 127 AA; 15162 MW; B5DA100D383E3547 CRC64;

Query Match 76.9%; Score 83; DB 1; Length 127;
Best Local Similarity 70.6%; Pred. No. 2.3e-05;
Matches 12; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 DCPSEWSSYEGFCYKPF 17
:|||||:
Db 3 ECPSGWSSYRYCYKPF 19
:|||||:

RESULT 5
BOTA_BOTJA
ID BOTA_BOTJA STANDARD; PRT; 133 AA.
AC P22029;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Botrocetin, alpha chain (platelet coagglutinin).
OS Bothrops jararaca (Jararaca).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Crotalinae; Bothrops.
OX NCBI_TaxID=8724;
RN [1]
RP SEQUENCE AND DISULFIDE BONDS.
RC TISSUE=Venom;
RX MEDLINE=93157385; PubMed=8430107;
RA Usami Y., Fujimura Y., Suzuki M., Ozeki Y., Nishio K., Fukui H.,
RA Titani K.;
RT "Primary structure of two-chain botrocetin, a von Willebrand factor
RT modulator purified from the venom of Bothrops jararaca.";

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Proc. Natl. Acad. Sci. U.S.A. 90:928-932(1993).
[2]
RN SEQUENCE OF 1-40.
RP TISSUE=Venom;
RX MEDLINE=91129280; PubMed=1993206;
RA Fujimura Y., Titani K., Usami Y., Suzuki M., Oyama R., Matsui T.,
RA Fukui H., Sugimoto M., Ruggeri Z.M.;
RT "Isolation and chemical characterization of two structurally and
RT functionally distinct forms of botrocetin, the platelet coagglutinin
RT isolated from the venom of Bothrops jararaca.";
RL Biochemistry 30:1957-1964(1991).
RN [3]
RP X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS).
RX MEDLINE=22118144; PubMed=12121649;
RA Fukuda K., Doggett T.A., Bankston L.A., Cruz M.A., Diacovo T.G.,
RA Liddington R.C.;
RT "Structural basis of von Willebrand factor activation by the snake
RT toxin botrocetin.";
RL Structure 10:943-950(2002).
CC -1- FUNCTION: Two-chain Botrocetin forms an activated complex with
CC VWF, and the complex then binds to platelet GPIb, resulting in
CC platelet agglutination.
CC -1- FUNCTION: There are two distinct forms of the von Willebrand
CC factor-dependent platelet coagglutinin. The dimeric form is
CC 34-times more active than the one-chain Botrocetin in promoting
CC VWF binding to platelets.
CC -1- SUBUNIT: Disulfide-linked dimer of an alpha and a beta chain.
CC VWF and Botrocetin form a soluble complex.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Contains 1 C-type lectin family domain.
DR PIR, A47267; A47267.
DR PDB, 1JJK; 17-JUL-02.
DR PDB, 1FVU; 14-FEB-01.
DR InterPro, IPR002353; AntifreezeZell.
DR InterPro, IPR001304; Lectin_C.
DR Pfam, PF00059; lectin_C; 1.
DR PRINTS, PR00356; ANTIFREEZEII.
DR SMART, SM00034; CLECT; 1.
DR PROSITE, PS00645; C_TYPE_LLECTIN_1; 1.
DR PROSITE, PS00041; C_TYPE_LLECTIN_2; 1.
KW Lectin; 3D-structure.
FT DISULFID 2 13
FT DISULFID 30 128
FT DISULFID 80 80 INTERCHAIN (WITH C-75 IN BETA CHAIN).
FT DISULFID 103 120
SQ SEQUENCE 133 AA; 15215 MW; B4CF4502946AC74B CRC64;

Query Match 75.0%; Score 81; DB 1; Length 133;
Best Local Similarity 82.4%; Pred. No. 4.8e-05;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 DCPSEWSSYEGFCYKPF 17
:|||||:
Db 1 DCPSGWSSYEGNCYKPF 17
:|||||:

RESULT 6
ABBB_TRIAB
ID ABBB_TRIAB STANDARD; PRT; 118 AA.
AC P81116;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Alboaggregin B beta subunit.
OS Trimeresurus albolabris (White-lipped pit viper).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Crotalinae; Trimeresurus.
OX NCBI_TaxID=8765;
RN [1]
RP SEQUENCE.
RC TISSUE=Venom;
RX MEDLINE=98189535; PubMed=9531050;

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RA Kowalska M.A., Tan L., Holt J.C., Peng M., Karczewski J.,
RA Calvete J.J., Niewiarowski S.;
RT "Alboaggregins A and B. Structure and interaction with human
platelets.";
RL Thromb. Haemost. 79:609-613(1998).
CC -1- FUNCTION: Binds to platelet GPIb/IX receptor system and stimulates
agglutination.
CC -1- SUBUNIT: Heterodimer of alpha and beta subunits, disulfide-linked.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Contains 1 C-type lectin family domain.
DR HSP; P23807; 11XX.
DR InterPro; IPR001304; Lectin C.
DR Pfam; PF00059; lectin_c; 1.
DR SMART; SM00034; CLECT_1.
DR PROSITE; PS00615; C_TYPE_LECTIN_1; FALSE_NEG.
DR PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
KW Lectin.
FT DOMAIN 1 118 C-TYPE LECTIN (LONG FORM).
FT DISULFID 2 13 BY SIMILARITY.
FT DISULFID 75 75 INTERCHAIN (WITH C-79 IN ALPHA CHAIN)
FT DISULFID 96 111 (BY SIMILARITY).
FT DISULFID 118 AA; 13794 MW; 059EDFF6B474C4CE CRC64;
SQ SEQUENCE 118 AA; 13794 MW; 059EDFF6B474C4CE CRC64;
Query Match 74.1%; Score 80; DB 1; Length 118;
Best Local Similarity 70.6%; Pred. No. 5.9e-05;
Matches 12; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
QY 1 DCPSEWSSYEGFCYKPF 17
DB 1 DCPSDWSSYDYCYKVF 17
RESULT 7
ABA3 TRIAB
ID ABA3 TRIAB STANDARD; PRT; 125 AA.
AC P8113;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Alboaggregin A subunit 3.
OS Trimeresurus albolabris (White-lipped pit viper).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Crotalinae; Trimeresurus.
OX NCBI_TaxID=8765;
RN [1]
RP SEQUENCE.
RC TISSUE=Venom;
RX MEDLINE=98189535; PubMed=9531050;
RA Kowalska M.A., Tan L., Holt J.C., Peng M., Karczewski J.,
RA Calvete J.J., Niewiarowski S.;
RT "Alboaggregins A and B. Structure and interaction with human
platelets.";
RL Thromb. Haemost. 79:609-613(1998).
CC -1- FUNCTION: Binds to platelet GPIb/IX receptor system and stimulates
agglutination.
CC -1- SUBUNIT: Heterotetramer of the subunits 1, 2, 3 and 4,
disulfide-linked.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Contains 1 C-type lectin family domain.
DR HSP; P23807; 11XX.
DR InterPro; IPR001304; Lectin C.
DR Pfam; PF00059; lectin_c; 1.
DR SMART; SM00034; CLECT_1.
DR PROSITE; PS00615; C_TYPE_LECTIN_1; FALSE_NEG.
DR PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
KW Lectin.
FT DOMAIN 3 123 C-TYPE LECTIN (LONG FORM).
FT DISULFID 4 15 BY SIMILARITY.
FT DISULFID 32 121 BY SIMILARITY.
FT DISULFID 98 113 BY SIMILARITY.
SQ SEQUENCE 125 AA; 14798 MW; CAPA24C098DF3293 CRC64;

Query Match 74.1%; Score 80; DB 1; Length 125;
Best Local Similarity 70.6%; Pred. No. 6.3e-05;
Matches 12; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
QY 1 DCPSEWSSYEGFCYKPF 17
DB 3 DCPFGWSSYEGYCKVY 19
RESULT 8
BOTB BOTJA
ID BOTB BOTJA STANDARD; PRT; 125 AA.
AC P22030;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Botrocetin, beta chain (Platelet coagglutinin).
OS Bothrops jararaca (Jararaca).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Crotalinae; Bothrops.
OX NCBI_TaxID=8724;
RN [1]
RP SEQUENCE, AND DISULFIDE BONDS.
RC TISSUE=Venom;
RX MEDLINE=93157385; PubMed=8430107;
RA Usami Y., Fujimura Y., Suzuki M., Ozeki Y., Nishio K., Fukui H.,
RA Titani K.;
RT "Primary structure of two-chain botrocetin, a von Willebrand factor
modulator purified from the venom of Bothrops jararaca.";
RL Proc. Natl. Acad. Sci. U.S.A. 90:928-932(1993).
RN [2]
RP SEQUENCE OF 1-40.
RC TISSUE=Venom;
RX MEDLINE=91129280; PubMed=1993206;
RA Fujimura Y., Titani K., Usami Y., Suzuki M., Oyama R., Matsui T.,
RA Fukui H., Sugimoto M., Ruggeri Z.M.;
RT "Isolation and chemical characterization of two structurally and
functionally distinct forms of botrocetin, the platelet coagglutinin
isolated from the venom of Bothrops jararaca.";
RL Biochemistry 30:1957-1964(1991).
RN [3]
RP X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS).
RX MEDLINE=22118144; PubMed=12121649;
RA Fukuda K., Doggett T.A., Bankston L.A., Cruz M.A., Diacovo T.G.,
RA Liddington R.C.;
RT "Structural basis of von Willebrand factor activation by the snake
toxin botrocetin.";
RL Structure 10:943-950(2002).
CC -1- FUNCTION: Two-chain Botrocetin forms an activated complex with
vWF, and the complex then binds to platelet GPIb, resulting in
platelet agglutination.
CC -1- FUNCTION: There are two distinct forms of the von Willebrand
factor-dependent platelet coagglutinin. The dimeric form is
34-times more active than the one-chain Botrocetin in promoting
vWF binding to platelets.
CC -1- SUBUNIT: Disulfide-linked dimer of an alpha and a beta chain.
CC vWF and Botrocetin form a soluble complex.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Contains 1 C-type lectin family domain.
DR PIR; B47267; B47267.
DR PDB; 1IJK; 17-JUL-02.
DR PDB; 1FVU; 14-FEB-01.
DR InterPro; IPR001304; Lectin C.
DR Pfam; PF00059; lectin_c; 1.
DR SMART; SM00034; CLECT_1.
DR PROSITE; PS00615; C_TYPE_LECTIN_1; FALSE_NEG.
DR PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
KW Lectin.
FT DISULFID 2 13
FT DISULFID 30 121
FT DISULFID 75 75 INTERCHAIN (WITH C-80 IN ALPHA CHAIN).

```

FT DISULFID 98 113
SQ SEQUENCE 125 AA; 15037 MW; 1ED2027ED817FC0A CRC64;

Query Match 73.1%; Score 79; DB 1; Length 125;
Best Local Similarity 70.6%; Pred. No. 8.8e-05;
Matches 12; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 DCPSEWSSYEGFCYKPF 17
   |||:|||||:|:|
Db 1 DCPDMSWSSYEGHCYRVF 17

RESULT 9
ABAI TRIAB STANDARD; PRT; 131 AA.
AC P8111;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Alboaggregin A subunit 1.
OS Trimeresurus albolabris (White-lipped pit viper).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Crotalinae; Trimeresurus.
OX NCBI_TaxID=8765;
RN [1]
RP SEQUENCE.
RC TISSUE=Venom;
RX MEDLINE=98189535; PubMed=9531050;
RA Kowalska M.A., Tan L., Holt J.C., Peng M., Karczewski J.,
RA Calvete J.J., Niewiarowski S.;
RT "Alboaggregins A and B. Structure and interaction with human
RT platelets."
RL Thromb. Haemost. 79:609-613(1998).
CC -1- FUNCTION: Binds to platelet GPIb/IX receptor system and stimulates
CC agglutination.
CC -1- SUBUNIT: Heterotetramer of the subunits 1, 2, 3 and 4,
CC disulfide-linked.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Contains 1 C-type lectin family domain.
DR HSP; P23806; IIXX.
DR InterPro; IPR001304; Lectin_C.
DR Pfam; PF00059; Lectin_C; 1.
DR SMART; SM00034; CLECT_1.
DR PROSITE; PS00615; C_TYPE_LLECTIN_1; 1.
DR PROSITE; PS50041; C_TYPE_LLECTIN_2; 1.
KW Lectin.
FT DOMAIN 1 129 C-TYPE LECTIN (LONG FORM).
FT DISULFID 2 13 BY SIMILARITY.
FT DISULFID 30 127 BY SIMILARITY.
FT DISULFID 102 119 BY SIMILARITY.
SQ SEQUENCE 131 AA; 15427 MW; B3569F5BF91F624 CRC64;

Query Match 73.1%; Score 79; DB 1; Length 131;
Best Local Similarity 64.7%; Pred. No. 9.1e-05;
Matches 11; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 DCPSEWSSYEGFCYKPF 17
   |||:|||||:|:|
Db 1 DCPDMSWSSYDQYCYRVF 17

RESULT 10
IXA TRIFL STANDARD; PRT; 152 AA.
AC P23806; Q91246;
DT 01-NOV-1991 (Rel. 20, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Coagulation factor IX/factor X-binding protein A chain precursor
DE (IX/X-BP).
OS Trimeresurus flavoviridis (Habu).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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OC OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Crotalinae; Trimeresurus.
OX NCBI_TaxID=88087;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96184662; PubMed=8645314;
RA Matsuzaki R., Yoshinara E., Yamada M., Shima K., Atoda H., Morita T.;
RT "cDNA cloning of IX/X-BP, a heterogeneous two-chain anticoagulant
RT protein from snake venom."
RL Biochem. Biophys. Res. Commun. 220:382-387(1996).
RN [2]
RP SEQUENCE OF 24-152.
RC TISSUE=Venom;
RX MEDLINE=91332000; PubMed=1831197;
RA Atoda H., Hyuga M., Morita T.;
RT "The primary structure of coagulation factor IX/factor X-binding
RT protein isolated from the venom of Trimeresurus flavoviridis.
RT Homology with asialoglycoprotein receptors, proteoglycan core
RT protein, tetranectin, and lymphocyte Fc epsilon receptor for
RT immunoglobulin E."
RL J. Biol. Chem. 266:14903-14911(1991).
RN [3]
RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).
RX MEDLINE=9731317; PubMed=9187649;
RA Mizuno H., Fujimoto Z., Koizumi M., Kano H., Atoda H., Morita T.;
RT "Structure of coagulation factors IX/X-binding protein, a heterodimer
RT of C-type lectin domains."
RL Nat. Struct. Biol. 4:438-441(1997).
CC -1- FUNCTION: ANTICOAGULANT PROTEIN WHICH BINDS WITH FACTOR IX AND
CC FACTOR X IN THE PRESENCE OF CALCIUM WITH A 1 TO 1 STOICHIOMETRY.
CC -1- SUBUNIT: HETERODIMER OF CHAINS A AND B LINKED BY A DISULFIDE BOND.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- MISCELLANEOUS: CALCIUM IS REQUIRED FOR LIGAND BINDING.
CC -1- SIMILARITY: Contains 1 C-type lectin family domain.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC -----
DR EMBL; D83331; BAA11887.1; -.
DR PIR; JC4690; JC4690.
DR PDB; 1IIX; 06-MAY-98.
DR InterPro; IPR001304; Lectin_C.
DR InterPro; IPR003990; Pancreatis_ac.
DR Pfam; PF00059; lectin_c; 1.
DR PRINTS; PR01504; ENCREATITSAP.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS00615; C_TYPE_LLECTIN_1; 1.
DR PROSITE; PS00615; C_TYPE_LLECTIN_2; 1.
DR Lectin; Calcium; Signal; 3D-structure.
FT SIGNAL 1 23
FT CHAIN 24 152 COAGULATION FACTOR IX/FACTOR X-BINDING
FT PROTEIN A CHAIN.
FT DOMAIN 24 152 C-TYPE LECTIN (LONG FORM).
FT DISULFID 25 36 BY SIMILARITY.
FT DISULFID 53 150 BY SIMILARITY.
FT DISULFID 102 102 BY SIMILARITY.
FT DISULFID 125 142 INTERCHAIN (WITH C-98 OF B CHAIN).
FT TURN 27 28 BY SIMILARITY.
FT STRAND 30 31
FT STRAND 36 44
FT HELIX 46 56
FT TURN 58 59
FT STRAND 61 62
FT HELIX 68 81
FT STRAND 89 95
FT STRAND 105 105
FT TURN 107 108
FT TURN 111 111

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FT STRAND 117 117
 FT HELIX 119 121
 FT STRAND 125 128
 FT HELIX 130 132
 FT TURN 133 134
 FT STRAND 137 140
 FT TURN 142 143
 FT STRAND 146 152
 SQ SEQUENCE 152 AA; 17213 MW; FB3DD02369009263 CRC64;

Query Match 70.4%; Score 76; DB 1; Length 152;
 Best Local Similarity 76.5%; Pred. No. 0.00029;
 Matches 13; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 DCPSEWSSYEGFCYKPF 17
 ||| ||||| |||||
 Db 24 DCLSGWSSYEGHCYKAF 40

RESULT 11

CVXB_CRODU STANDARD; PRT; 148 AA.
 AC 093427;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Convulxin beta precursor (CVX beta).
 OS Crotalus durissus terrificus (South American rattlesnake).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroides;
 OC Viperidae; Crotalinae; Crotalus.
 OC NCBI_TaxID=8732;
 RN [1]
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 24-53; 99-109 AND 126-145.
 RC TISSUE=Venom gland;
 RA MEDLINE=98324901; PubMed=9657980;
 RX Leduc M., Bon C.;
 RT "Cloning of subunits of convulxin, a collagen-like platelet-
 aggregating protein from Crotalus durissus terrificus venom.";
 RL Biochem. J. 333:389-393(1998).
 CC -!- FUNCTION: Binds to the platelet and collagen receptor,
 Glycoprotein VI (GPVI).
 CC -!- SUBUNIT: Heterodimer of three alpha chains and three beta
 chains; disulfide-linked.
 CC -!- SIMILARITY: Contains 1 C-type lectin family domain.
 CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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 or send an email to license@sb-sib.ch).
 CC
 CC EMBL; Y16349; CAA76182.1; -;
 DR HSSP; P23807; IIXX.
 DR InterPro: IPR001304; LECTIN_C.
 DR Pfam; PF00059; lectin_c; 1.
 DR SMART; SM00034; CLECT; 1.
 DR PROSITE; PS00615; C_TYPE_LLECTIN_1; 1.
 DR PROSITE; PS00041; C_TYPE_LLECTIN_2; 1.
 DR LECTIN; Glycoprotein; Signal.
 FT SIGNAL 1 23
 FT CHAIN 24 148
 FT DOMAIN 34 145
 FT DISULFID 26 26
 FT INTERCHAIN (WITH C-158 IN ALPHA CHAIN)
 FT (POTENTIAL).
 FT BY SIMILARITY.
 FT DISULFID 27 38
 FT DISULFID 55 144
 FT DISULFID 100 100
 FT INTERCHAIN (WITH C-104 IN ALPHA CHAIN)
 FT (POTENTIAL).
 FT BY SIMILARITY.
 FT DISULFID 121 136
 SQ SEQUENCE 148 AA; 17402 MW; 94D7E3E1BC693B9F CRC64;

Query Match 68.5%; Score 74; DB 1; Length 148;
 Best Local Similarity 68.8%; Pred. No. 0.00054;
 Matches 11; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 2 CDPSEWSSYEGFCYKPF 17
 ||| ||||| |||||
 Db 27 CDPHSSYDRYCYKVF 42

RESULT 12

RHCA_AGRKH STANDARD; PRT; 133 AA.
 AC P81397;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Rhodocetin alpha subunit.
 OS Agkistrodon rhodostoma (Malayan pit viper) (Calloselasma rhodostoma).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroides;
 OC Viperidae; Crotalinae; Calloselasma.
 OC NCBI_TaxID=8717;
 RN [1]
 RP SEQUENCE, FUNCTION, SUBUNIT, AND MASS SPECTROMETRY.
 RC TISSUE=Venom;
 RA MEDLINE=99303998; PubMed=10360956;
 RX Wang R., Kini R.M., Chung M.C.M.;
 RT "Rhodocetin, a novel platelet aggregation inhibitor from the venom of
 Calloselasma rhodostoma (Malayan pit viper): synergistic and
 noncovalent interaction between its subunits.";
 RL Biochemistry 38:7584-7593(1999).
 CC -!- FUNCTION: A potent inhibitor of collagen-induced platelet
 aggregation. Individually, neither subunit inhibits platelet
 aggregation. Both subunits are essential.
 CC -!- SUBUNIT: Heterodimer of one alpha and one beta subunit held
 together by noncovalent interactions rather than by intersubunit
 disulfide bridges.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- MASS SPECTROMETRY: MW=15955.90; MW ERR=1.44; METHOD=Electrospray.
 CC -!- SIMILARITY: Contains 1 C-type lectin family domain.
 DR HSSP; P23806; IIXX.
 DR InterPro: IPR001304; LECTIN_C.
 DR Pfam; PF00059; lectin_c; 1.
 DR SMART; SM00034; CLECT; 1.
 DR PROSITE; PS00615; C_TYPE_LLECTIN_1; FALSE NEG.
 DR PROSITE; PS00041; C_TYPE_LLECTIN_2; 1.
 DR LECTIN.
 DR DOMAIN 1 129 C-TYPE LECTIN (LONG FORM).
 FT DISULFID 2 13 BY SIMILARITY.
 FT DISULFID 30 127 BY SIMILARITY.
 FT DISULFID 102 119 BY SIMILARITY.
 SQ SEQUENCE 133 AA; 15962 MW; 386EAC519DFC674D CRC64;

Query Match 66.7%; Score 72; DB 1; Length 133;
 Best Local Similarity 58.8%; Pred. No. 0.00095;
 Matches 10; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 DCPSEWSSYEGFCYKPF 17
 ||| ||||| |||||
 Db 1 DCPDGWSSYKSYCYRPF 17

RESULT 13

ABBA_TRIAB STANDARD; PRT; 132 AA.
 ID ABBA_TRIAB
 AC P81115;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Alboaggregin B alpha subunit.
 OS Trimeresurus albolabris (White-lipped pit viper).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidae;
 OC Viperidae; Crotalinae; Trimeresurus.
 RN NCBI_TaxID=8765;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Venom;
 RX MEDLINE=98189535; PubMed=9531050;
 RA Kowaleka M.A., Tan L., Holt J.C., Peng M., Karczewski J.,
 RA Calvete J.J., Niewiarowski S.;
 RT "Alboaggregins A and B. Structure and interaction with human
 RT platelets.";
 RL Thromb. Haemost. 79:609-613(1998).
 CC -!- FUNCTION: Binds to platelet GPIb/IX receptor system and stimulates
 CC agglutination.
 CC -!- SUBUNIT: Heterodimer of alpha and beta subunits, disulfide-linked.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: Contains 1 C-type lectin family domain.
 DR HSSP; P23806; 11XX.
 DR InterPro; IPR001304; Lectin_C.
 DR Pfam; PF00059; lectin_c; 1.
 DR SMART; SM00034; CLECT; 1.
 DR PROSITE; PS00615; C_TYPE_LECTIN_1; 1.
 DR PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
 KW Lectin.
 FT DOMAIN 1 129 C-TYPE LECTIN (LONG FORM).
 FT DISULFID 2 13 BY SIMILARITY.
 FT DISULFID 30 127 BY SIMILARITY.
 FT DISULFID 79 79 INTERCHAIN (WITH C-75 IN BETA CHAIN)
 FT (BY SIMILARITY).
 FT DISULFID 102 119 BY SIMILARITY.
 SQ SEQUENCE 132 AA; 15419 MW; 6FAE64820383F16F CRC64;
 Query Match 63.9%; Score 69; DB 1; Length 132;
 Best Local Similarity 60.0%; Pred. No. 0.0026;
 Matches 9; Conservative 5; Mismatches 1; Indels 0; Gaps 0;
 QY 1 DCPSEWSSYEGFCYK 15
 DB 1 DCPDWSSEFKQYCYQ 15
 RESULT 14
 ECHB_ECHCA
 ID ECHB_ECHCA STANDARD; PRT; 123 AA.
 AC P81996;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Echicetin beta subunit.
 OS Echis carinatus (Saw-scaled viper).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidae;
 OC Viperidae; Viperinae; Echis.
 OX NCBI_TaxID=40353;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Venom;
 RX MEDLINE=95091801; PubMed=7999097;
 RA PENG M., Holt J.C., Niewiarowski S.;
 RT "Isolation, characterization and amino acid sequence of echicetin beta
 RT subunit, a specific inhibitor of von Willebrand factor and thrombin
 RT interaction with glycoprotein Ib.";
 RL Biochem. Biophys. Res. Commun. 205:68-72(1994).
 RN [2]
 RP SEQUENCE OF 1-30.
 RC TISSUE=Venom;
 RX MEDLINE=97250657; PubMed=9163349;
 RA Polgar J., Magnanat E.M., Peitsch M.C., Wells T.N.C., Sagi M.S.A.,
 RA Clemetson K.J.;
 RT "Amino acid sequence of the alpha subunit and computer modelling of
 RT the alpha and beta subunits of echicetin from the venom of Echis
 RT carinatus (saw-scaled viper).";
 RL Biochem. J. 323:533-537(1997).

RN [3]
 RP CHARACTERIZATION.
 RC TISSUE=Venom;
 RX MEDLINE=93244424; PubMed=8481512;
 RA Peng M., Lu W., Bevilgia L., Niewiarowski S., Kirby E.P.;
 RT "Echicetin: a snake venom protein that inhibits binding of von
 RT Willebrand factor and alboaaggregins to platelet glycoprotein Ib.";
 RL Blood 81:2321-2328(1993).
 CC -!- FUNCTION: Binds to platelet GPIb and inhibits platelet
 CC agglutination.
 CC -!- SUBUNIT: Heterodimer of alpha and beta subunits.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: Contains 1 C-type lectin family domain.
 DR PIR; JC2415; JC2415.
 DR HSSP; P23807; 11XX.
 DR InterPro; IPR001304; Lectin_C.
 DR Pfam; PF00059; lectin_c; 1.
 DR SMART; SM00034; CLECT; 1.
 DR PROSITE; PS00615; C_TYPE_LECTIN_1; 1.
 DR PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
 KW Lectin.
 FT DOMAIN 1 121 C-TYPE LECTIN (LONG FORM).
 FT DISULFID 2 13 BY SIMILARITY.
 FT DISULFID 30 119 BY SIMILARITY.
 FT DISULFID 75 75 INTERCHAIN (WITH C-81 IN ALPHA CHAIN) (BY
 FT SIMILARITY).
 FT DISULFID 96 111 BY SIMILARITY.
 SQ SEQUENCE 123 AA; 14869 MW; C42C0AD7CDE18CA6 CRC64;
 Query Match 62.0%; Score 67; DB 1; Length 123;
 Best Local Similarity 58.8%; Pred. No. 0.0047;
 Matches 10; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
 QY 1 DCPSEWSSYEGFCYKPF 17
 DB 1 NCLPDWSVYEGCYKVPF 17
 RESULT 15
 RHCB_AGRKH
 ID RHCB_AGRKH STANDARD; PRT; 129 AA.
 AC P81398;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Rhodocetin beta subunit.
 OS Agkistrodon rhodostoma (Malayan pit viper) (Calloselasma rhodostoma).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidae;
 OC Viperidae; Crotalinae; Calloselasma.
 OX NCBI_TaxID=8717;
 RN [1]
 RP SEQUENCE, FUNCTION, SUBUNIT, AND MASS SPECTROMETRY.
 RC TISSUE=Venom;
 RX MEDLINE=93303998; PubMed=10360956;
 RA Wang R., Kini R.M., Chung M.C.M.;
 RT "Rhodocetin, a novel platelet aggregation inhibitor from the venom of
 RT Calloselasma rhodostoma (Malayan pit viper): synergistic and
 RT noncovalent interaction between its subunits.";
 RL Biochemistry 38:7584-7593(1999).
 CC -!- FUNCTION: A potent inhibitor of collagen-induced platelet
 CC aggregation. Individually, neither subunit inhibits platelet
 CC aggregation. Both subunits are essential.
 CC -!- SUBUNIT: Heterodimer of one alpha and one beta subunit held
 CC together by noncovalent interactions rather than by intersubunit
 CC disulfide bridges.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- MASS SPECTROMETRY: MW=15184.53; MW_ERR=2.74; METHOD=Electrospray.
 CC -!- SIMILARITY: Contains 1 C-type lectin family domain.
 DR HSSP; P23806; 11XX.
 DR InterPro; IPR001304; Lectin_C.
 DR Pfam; PF00059; lectin_c; 1.
 DR SMART; SM00034; CLECT; 1.

DR PROSITE; PS00615; C-TYPE LECTIN 1; FALSE-NEG.
KW LECTIN; PS00041; C-TYPE LECTIN_2; 1.
FT DOMAIN 3 125 C-TYPE LECTIN (LONG FORM).
FT DISULFID 4 15 BY SIMILARITY.
FT DISULFID 98 115 BY SIMILARITY.
SQ SEQUENCE 129 AA; 15190 MW; EF4B318FAAC807AE CRC64;
Query Match 59.3%; Score 64; DB 1; Length 129;
Best Local Similarity 56.2%; Pred. NO. 0.013;
Matches 9; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 2 CPSEWSYEGFCYKPF 17
||: ||: : |||||
Db 4 CPTWSASKLYCYKPF 19

Search completed: December 8, 2003, 09:53:10
Job time : 2.56762 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 8, 2003, 09:49:24 ; Search time 8.25714 Seconds
(without alignments)
531.285 Million cell updates/sec.

Title: US-09-938-114-4

Perfect score: 108
Sequence: 1 DCPSEWSYEGFCYKPF 17

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SPTREMBL 23:**

1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mic:*
8: sp_organelle:*
9: sp_phase:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	101	93.5	146	13 Q8JIW1	Q8jiw1 agkistrodon
2	98	90.7	124	13 Q98SM5	Q98sm5 agkistrodon
3	98	90.7	146	13 Q9IAM0	Q9iam0 agkistrodon
4	98	90.7	146	13 Q9DEF8	Q9def8 agkistrodon
5	98	90.7	146	13 Q8JIV7	Q8jiv7 agkistrodon
6	94	87.0	146	13 Q9DG31	Q9dg31 agkistrodon
7	94	87.0	146	13 Q9I840	Q9i840 agkistrodon
8	93	86.1	146	13 Q8AYH4	Q8ayh4 agkistrodon
9	86	79.6	146	13 Q9YI92	Q9yi92 agkistrodon
10	84	77.8	145	13 Q9PS05	Q9ps05 bothrops ja
11	84	77.8	145	13 Q9YGN4	Q9ygn4 agkistrodon
12	81	75.0	30	13 Q9PS06	Q9ps06 bothrops ja
13	80	74.1	152	13 Q9DEF9	Q9def9 agkistrodon
14	80	74.1	152	13 Q8JIW0	Q8jiw0 agkistrodon
15	79	73.1	152	13 Q9DG39	Q9dg39 agkistrodon
16	78	72.2	124	13 Q90WL9	Q90wl9 agkistrodon

17	78	72.2	155	13 Q8JIV8	Q8jiv8 agkistrodon
18	77	71.3	40	13 Q9PS20	Q9ps20 trimeresuru
19	77	71.3	152	13 Q9IAM1	Q9iam1 agkistrodon
20	76	70.4	33	13 Q9PRQ7	Q9prq7 bothrops ja
21	76	70.4	123	13 Q9PSM5	Q9psm5 bothrops ja
22	76	70.4	146	13 Q98UJ0	Q98uj0 trimeresuru
23	73	67.6	146	13 Q9DEA1	Q9dea1 agkistrodon
24	71	65.7	157	13 Q9YGG9	Q9ygg9 agkistrodon
25	69	63.9	40	13 Q9PS19	Q9ps19 trimeresuru
26	66	61.1	42	13 Q9PRQ8	Q9prq8 bothrops ja
27	66	61.1	142	13 Q9PSM6	Q9psm6 bothrops ja
28	66	61.1	149	13 Q8UVC7	Q8uvc7 agkistrodon
29	66	61.1	149	13 Q8AYA3	Q8aya3 agkistrodon
30	66	61.1	151	13 Q8JIW2	Q8jiw2 agkistrodon
31	66	61.1	155	13 Q9DEA2	Q9dea2 agkistrodon
32	65	60.2	30	13 Q9PRP8	Q9prp8 echis carin
33	65	60.2	131	13 Q9PSM9	Q9psm9 echis carin
34	62	57.4	1152	13 Q90WM2	Q90wm2 xenopus lae
35	61	56.5	155	13 Q8JIV6	Q8jiv6 agkistrodon
36	60	55.6	30	13 Q9PRP7	Q9prp7 echis carin
37	58	53.7	16	13 Q9PRZ4	Q9prz4 bothrops ja
38	58	53.7	37	13 Q9PRT1	Q9prt1 trimeresuru
39	58	53.7	146	13 Q8JGT6	Q8jgt6 trimeresuru
40	58	53.7	148	13 Q8AV98	Q8av98 trimeresuru
41	58	53.7	149	5 Q02582	Q02582 inciliaria f
42	58	53.7	154	13 Q9YGN5	Q9ygn5 agkistrodon
43	57	52.8	34	13 Q9PRT2	Q9prt2 trimeresuru
44	57	52.8	158	13 Q8UVC6	Q8uvc6 agkistrodon
45	57	52.8	158	13 Q8JGT7	Q8jgt7 trimeresuru

ALIGNMENTS

RESULT 1
Q8JIW1
ID Q8JIW1 PRELIMINARY; PRT; 146 AA.
AC Q8JIW1
DT 01-OCT-2002 (TREMBLrel. 22, Created)
DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Agkisacutacin B-chain.
OS Agkistrodon acutus (Hundred-pace snake) (Deinagkistrodon acutus).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidae;
OC Viperidae; Crotalinae; Deinagkistrodon.
OX NCBI_TaxID=36307;
RN [1]
RP SEQUENCE FROM N.A.
RA Yu H., Xiang K., Wang Y., Liu J.;
RT "B chain of agkisacutacin from Deinagkistrodon acutus.";
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY091756; AAM22785.1; -
DR InterPro; IPR001304; Lectin C.
DR InterPro; IPR003990; Pancreatiss_ac.
DR Pfam; PF00059; lectin_C; 1.
DR PRINTS; PR01504; PNCREATITSAP.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS00615; C_TYPE_LLECTIN_1; 1.
DR PROSITE; PS00041; C_TYPE_LLECTIN_2; 1.
SQ SEQUENCE 146 AA; 16740 MW; 626086D68741317C CRC64;

Query Match 93.5%; Score 101; DB 13; Length 146;
Best Local Similarity 94.1%; Pred. No. 9.3e-08;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DCPSEWSYEGFCYKPF 17

Db 24 DCPSEWSYEGFCYKPF 40

RESULT 2
Q98SM5

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ID Q98SM5 PRELIMINARY; PRT; 124 AA.
AC Q98SM5;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Agkisacin-b.
OS Agkistrodon acutus (Hundred-pace snake) (Deinagkistrodon acutus).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Crotalinae; Deinagkistrodon.
OX NCBI_TaxID=36307;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Venom gland;
RA Zha X., Xu K.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF350324; AAK26430.1; -.
DR HSP; P23807; I1XX.
DR InterPro; IPR001304; Lectin_C.
DR Pfam; PF00059; lectin_c; 1.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS00615; C_TYPE_LECTIN_1; 1.
DR PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
SQ SEQUENCE 124 AA; 14701 MW; 4682DSE0CB3DC518 CRC64;

Query Match 90.7%; Score 98; DB 13; Length 124;
Best Local Similarity 88.2%; Pred. No. 2.3e-07;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DCPSEWSYEGFCYKPF 17
Db 2 DCPSDWSYEGHCYKPF 18

RESULT 3
Q91AM0 PRELIMINARY; PRT; 146 AA.
ID Q91AM0;
AC Q91AM0;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Agkisacutacin B chain.
OS Agkistrodon acutus (Hundred-pace snake) (Deinagkistrodon acutus).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Crotalinae; Deinagkistrodon.
OX NCBI_TaxID=36307;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=venom;
RA Cheng X., Qian Y., Liu Q., Li B.X.Y., Ding J., Xu Z., Huang W.,
RA Liu J.;
RL "Agkisacutacin, a new fibrinolytic & anti-platelet protein from
RL Agkistrodon acutus venom.";
DR EMBL; AF176421; AAF26287.1; -.
DR HSP; P23807; I1XX.
DR InterPro; IPR001304; Lectin_C.
DR InterPro; IPR003990; Pancreatiss_ac.
DR Pfam; PF00059; lectin_c; 1.
DR PRINTS; PR01504; PNCREATITSAP.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS00615; C_TYPE_LECTIN_1; 1.
DR PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
SQ SEQUENCE 146 AA; 16726 MW; 7360B6D6864131BB CRC64;

Query Match 90.7%; Score 98; DB 13; Length 146;
Best Local Similarity 88.2%; Pred. No. 2.7e-07;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DCPSEWSYEGFCYKPF 17
Db 24 DCPSDWSYEGHCYKPF 40

RESULT 4
Q9DEF8 PRELIMINARY; PRT; 146 AA.
ID Q9DEF8;
AC Q9DEF8;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Anticoagulant protein-B precursor.
GN ACP-B.
OS Agkistrodon acutus (Hundred-pace snake) (Deinagkistrodon acutus).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Crotalinae; Deinagkistrodon.
OX NCBI_TaxID=36307;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Venom gland;
RA Tani A., Nose T., Nikandrov N.N., Ogawa T., Deshimaru M., Fukumaki Y.,
RA Chang C., Shimohigashi Y., Ohno M.;
RL "Purification, sequencing, and cDNA cloning of a heterodimeric
RL anticoagulant protein from Deinagkistrodon actus venom gland.";
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB036881; BAB20441.1; -.
DR HSP; P23807; I1XX.
DR InterPro; IPR001304; Lectin_C.
DR InterPro; IPR003990; Pancreatiss_ac.
DR Pfam; PF00059; lectin_c; 1.
DR PRINTS; PR01504; PNCREATITSAP.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS00615; C_TYPE_LECTIN_1; 1.
DR PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
KW Signal.
FT SIGNAL 1 23 POTENTIAL.
SQ SEQUENCE 146 AA; 16997 MW; 420D71EBB4E9F5D2 CRC64;

Query Match 90.7%; Score 98; DB 13; Length 146;
Best Local Similarity 88.2%; Pred. No. 2.7e-07;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DCPSEWSYEGFCYKPF 17
Db 24 DCPSDWSYEGHCYKPF 40

RESULT 5
Q8JIV7 PRELIMINARY; PRT; 146 AA.
ID Q8JIV7;
AC Q8JIV7;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE ACF 1/2 B-chain.
OS Agkistrodon acutus (Hundred-pace snake) (Deinagkistrodon acutus).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Crotalinae; Deinagkistrodon.
OX NCBI_TaxID=36307;
RN [1]
RP SEQUENCE FROM N.A.
RA Yu H., Xiang K., Wang Y., Liu J.;
RL "B chain of ACF 1/2 from Deinagkistrodon acutus.";
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY091761; AAM22789.1; -.
DR InterPro; IPR001304; Lectin_C.
DR InterPro; IPR003990; Pancreatiss_ac.
DR Pfam; PF00059; lectin_c; 1.
DR PRINTS; PR01504; PNCREATITSAP.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS00615; C_TYPE_LECTIN_1; 1.
DR PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
SQ SEQUENCE 146 AA; 16925 MW; F2493CACBA5D2144 CRC64;

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Query Match      90.7%; Score 98; DB 13; Length 146;
Best Local Similarity 88.2%; Pred. No. 2.7e-07;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 DCPSEWSSVEGFCYKPF 17
DB 24 DCPGWSWSSYEGHCYKPF 40

RESULT 6
QSDG31 PRELIMINARY; PRT; 146 AA.
AC Q9DG31;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Halysin B-chain precursor.
OS Agkistrodon halys pallas (Chinese water moccasin) (Gloydius halys pallas).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Crotalinae; Gloydius.
OX NCBI_TaxID=8714;
RN [1];
RP SEQUENCE FROM N.A.
RC TISSUE=Venom;
RA Koo B.H., Sohn Y.D., Kim D.S., Jang Y.S., Chung K.H.;
RT "A Novel Coagulation Factor Xa Inhibitor from Korean Snake (Agkistrodon halys) venom.";
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF197915; AAG28522.1; -.
DR HSSP; P23807; 11XX.
DR InterPro; IPR001304; Lectin C.
DR InterPro; IPR001390; Pancreatiss_ac.
DR Pfam; PF00059; lectin c; 1.
DR PRINTS; PR01504; PNCEATITSP.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS00615; C_TYPE_LECTIN_1; 1.
DR PROSITE; PS00041; C_TYPE_LECTIN_2; 1.
FT NON_TER 146
SQ SEQUENCE 146 AA; 16770 MW; 930839140CFD8908 CRC64;

Query Match      87.0%; Score 94; DB 13; Length 146;
Best Local Similarity 88.2%; Pred. No. 1.1e-06;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 DCPSEWSSVEGFCYKPF 17
DB 24 DCPGWSWSSYEGHCYKPF 40

RESULT 8
Q8AY44 PRELIMINARY; PRT; 146 AA.
AC Q8AY44;
DT 01-MAR-2003 (TREMBLrel. 23, Created)
DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Agglucetin-beta 1 subunit precursor.
OS Agkistrodon acutus (Hundred-pace snake) (Deinagkistrodon acutus).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Crotalinae; Deinagkistrodon.
OX NCBI_TaxID=36307;
RN [1];
RP SEQUENCE FROM N.A.
RX MEDLINE=21542539; PubMed=11686327;
RA Wang W.-J., Huang T.F.;
RT "A novel tetrameric venom protein, agglucetin from Agkistrodon acutus, acts as a glycoprotein Ib agonist.";
RL Thromb. Haemost. 86:1077-1086(2001).
RN [2];
RP SEQUENCE FROM N.A.
RA Wang W.-J., Ling Q.-D., Huang T.-F.;
RT "Molecular structure and functional characterization of agglucetin, a tetrameric glycoprotein Ib-binding protein, from Formosan pit viper.";
RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF540647; AAN23126.1; -.
KW Signal.
FT SIGNAL 1 23 POTENTIAL.
FT CHAIN 24 146 AGGLUCETIN-BETA 1 SUBUNIT.
SQ SEQUENCE 146 AA; 16728 MW; 2342BAE39EB0CCB9 CRC64;

Query Match      86.1%; Score 93; DB 13; Length 146;
Best Local Similarity 88.2%; Pred. No. 1.5e-06;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 DCPSEWSSVEGFCYKPF 17
DB 24 DCPGWSWSSYEGHCYKPF 40

RESULT 9
Q9YI92 PRELIMINARY; PRT; 146 AA.
ID Q9YI92
RA Chung C.H., Au L.C., Huang T.F.;
RT "Molecular cloning and sequence analysis of aggretin, a collagen-like

```

DT 01-MAY-1999 (TrEMBLrel. 10, Created)
 DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
 DE Mamushigin beta.
 OS Agkistrodon halys blomhoffii (Mamushi) (Gloydius blomhoffii).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidodactylus; Squamata; Scleroglossa; Serpentes; Colubroidea;
 OC Viperidae; Crotalinae; Agkistrodon.
 OX NCBI_TaxID=61300;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98319530; PubMed=9657448;
 RA Sakurai Y., Fujimura Y., Kokubo T., Inamura K., Kawasaki T., Handa M.,
 RA Suzuki M., Matsui T., Tani K., Yoshioka A.,
 RT "The cDNA cloning and molecular characterization of a snake venom
 RT platelet glycoprotein IB-binding protein, mamushigin, from Agkistrodon
 RT halys blomhoffii venom.";
 RL Thromb. Haemost. 79:1199-1207(1998).
 DR EMBL; AB019616; BAA34425.1; -
 DR HSP; P23807; IXX.
 DR InterPro; IPR001304; Lectin_C.
 DR Pfam; PF00059; lectin_c; 1.
 DR SMART; SM00034; CLECT; 1.
 DR PROSITE; PS00615; C TYPE LECTIN 1; 1.
 DR PROSITE; PS00041; C TYPE LECTIN 2; 1.
 DR PROSITE; PS00041; C TYPE LECTIN 2; 1.
 SQ SEQUENCE 146 AA; 17064 MW; 9EDA84BDC24E76D CRC64;

Query Match 79.6%; Score 86; DB 13; Length 146;
 Best Local Similarity 76.5%; Pred. No. 1.7e-05;
 Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 DCPSEWSSVYEGFCYKPF 17
 |||||:|||||:|
 DB 24 DCPSEWSSVYEGHCYRVF 40

RESULT 10

Q9PS05 PRELIMINARY; PRT; 30 AA.
 AC Q9PS05;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
 DE Factor IX/factor X-binding protein A chain (Fragment).
 OS Bothrops jararaca (Jararaca).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidodactylus; Squamata; Scleroglossa; Serpentes; Colubroidea;
 OC Viperidae; Crotalinae; Bothrops.
 OX NCBI_TaxID=8724;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=93326575; PubMed=8334120;
 RA Sekiya F., Atoda H., Morita T.;
 RT "Isolation and characterization of an anticoagulant protein homologous
 RT to botrocetin from the venom of Bothrops jararaca.";
 RL Biochemistry 32:6892-6897(1993).
 DR HSP; P23807; IXX.
 SQ SEQUENCE 30 AA; 3709 MW; DD49A218EDDBA9D2 CRC64;

Query Match 77.8%; Score 84; DB 13; Length 30;
 Best Local Similarity 76.5%; Pred. No. 7.7e-06;
 Matches 13; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 DCPSEWSSVYEGFCYKPF 17
 |||||:|||||:|
 DB 1 DCPSEWSSVYEGHCYRVF 17

RESULT 11

Q9YGN4 PRELIMINARY; PRT; 145 AA.
 AC Q9YGN4;
 DT 01-MAY-1999 (TrEMBLrel. 10, Created)

DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
 DT 01-MAY-2003 (TrEMBLrel. 23, Last annotation update)
 DE Fibrinogen clotting inhibitor B chain.
 OS Agkistrodon halys brevicaudus (Korean slamosa snake) (Gloydius halys
 OS brevicaudus).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidodactylus; Squamata; Scleroglossa; Serpentes; Colubroidea;
 OC Viperidae; Crotalinae; Gloydius.
 OX NCBI_TaxID=66175;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Kim D.S., Koh Y.S.;
 RT "Purification and molecular cloning of snake venom fibrin clotting
 RT inhibitor.";
 RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF125310; AAD18056.1; -
 DR HSP; P23807; IXX.
 DR InterPro; IPR001304; Lectin_C.
 DR InterPro; IPR003990; Pancreatitis_ac.
 DR Pfam; PF00059; lectin_c; 1.
 DR PRINTS; PR01504; PNCREATITSAP.
 DR SMART; SM00034; CLECT; 1.
 DR PROSITE; PS00615; C TYPE LECTIN 1; 1.
 DR PROSITE; PS00041; C TYPE LECTIN 2; 1.
 DR PROSITE; PS00041; C TYPE LECTIN 2; 1.
 SQ SEQUENCE 145 AA; 16746 MW; 6FFC67E2C1F20BC8 CRC64;

Query Match 77.8%; Score 84; DB 13; Length 145;
 Best Local Similarity 82.4%; Pred. No. 3.5e-05;
 Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 DCPSEWSSVYEGFCYKPF 17
 |||||:|||||:|
 DB 24 DCPSEWSSVYEGHCYRVF 40

RESULT 12

Q9PS06 PRELIMINARY; PRT; 30 AA.
 AC Q9PS06;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
 DE Factor IX/factor X-binding protein B chain (Fragment).
 OS Bothrops jararaca (Jararaca).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidodactylus; Squamata; Scleroglossa; Serpentes; Colubroidea;
 OC Viperidae; Crotalinae; Bothrops.
 OX NCBI_TaxID=8724;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=93326575; PubMed=8334120;
 RA Sekiya F., Atoda H., Morita T.;
 RT "Isolation and characterization of an anticoagulant protein homologous
 RT to botrocetin from the venom of Bothrops jararaca.";
 RL Biochemistry 32:6892-6897(1993).
 DR HSP; P23807; IXX.
 SQ SEQUENCE 30 AA; 3506 MW; 14A2DFFB41F2B6F5 CRC64;

Query Match 75.0%; Score 81; DB 13; Length 30;
 Best Local Similarity 70.6%; Pred. No. 2.2e-05;
 Matches 12; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 DCPSEWSSVYEGFCYKPF 17
 |||||:|||||:|
 DB 1 DCPSEWSSVYEGHCYRVF 17

RESULT 13

Q9DEF9 PRELIMINARY; PRT; 152 AA.
 AC Q9DEF9;
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)

DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Anticoagulant protein A precursor.
GN ACP-A.
OS Agkistrodon acutus (Hundred-pace snake) (Deinagkistrodon acutus).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroides;
OC Viperidae; Crotalinae; Deinagkistrodon.
OX NCBI_TaxID=36307;
GN NCBI_TaxID=36307;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Venom gland;
RA Ogawa T., Tani A.;
RT "Purification, Sequencing, and cDNA Cloning of a Heterodimeric
RT Anticoagulant Protein from Agkistrodon actus Venom Gland.";
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB036880; BAA99281.1; -
DR HSSP; P23806; IIXX.
DR InterPro; IPR001304; LECTIN_C.
DR Pfam; PF00059; lectin_c; 1.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS00615; C_TYPE_LECTIN_1; 1.
DR PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
KW Signal.
FT SIGNAL 1 23 POTENTIAL.
SQ SEQUENCE 152 AA; 17124 MW; 5C59C0F503A4D223 CRC64;

Query Match 74.1%; Score 80; DB 13; Length 152;
Best Local Similarity 76.5%; Pred. No. 0.00015;
Matches 13; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 DCPSEWSSYEGFCYKPF 17
||| ||||| |||||
Db 24 DCSSWSSYEGHCYKAF 40

RESULT 14

ID Q8JIW0 PRELIMINARY; PRT; 152 AA.
AC Q8JIW0;
DT 01-OCT-2002 (TREMBlrel. 22, Created)
DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE ACF 1/2 A-chain.
OS Agkistrodon acutus (Hundred-pace snake) (Deinagkistrodon acutus).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroides;
OC Viperidae; Crotalinae; Deinagkistrodon.
OX NCBI_TaxID=36307;
RN [1]
RP SEQUENCE FROM N.A.
RA Yu H., Xiang K., Wang Y., Liu J.;
RT "A chain of ACF 1/2 from Deinagkistrodon acutus.";
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY091758; AAM22786.1; -
DR InterPro; IPR001304; LECTIN_C.
DR InterPro; IPR003990; Pancreatins_ac.
DR Pfam; PF00059; lectin_c; 1.
DR PRINTS; PR01504; PNCREATITSAP.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS00615; C_TYPE_LECTIN_1; 1.
DR PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
SQ SEQUENCE 152 AA; 17108 MW; B0870F3DA0A4D23B CRC64;

Query Match 74.1%; Score 80; DB 13; Length 152;
Best Local Similarity 76.5%; Pred. No. 0.00015;
Matches 13; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 DCPSEWSSYEGFCYKPF 17
||| ||||| |||||
Db 24 DCSSWSSYEGHCYKAF 40

RESULT 15

Q9DG39 PRELIMINARY; PRT; 152 AA.
ID Q9DG39;
AC Q9DG39;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Halysin A-chain precursor.
GN HXNA.
OS Agkistrodon halys pallas (Chinese water moccasin) (Gloydius halys pallas).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroides;
OC Viperidae; Crotalinae; Gloydius.
OX NCBI_TaxID=8714;
RN [1]
RP SEQUENCE FROM N.A.
RA Koo B.H., Sohn Y.D., Kim D.S., Jang Y.S., Chung K.H.;
RT "A novel coagulation factor Xa inhibitor from Korean snake
RT (Agkistrodon halys) venom.";
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF190827; AAGL7178.1; -
DR HSSP; P23806; IIXX.
DR InterPro; IPR001304; LECTIN_C.
DR InterPro; IPR003990; Pancreatins_ac.
DR Pfam; PF00059; lectin_c; 1.
DR PRINTS; PR01504; PNCREATITSAP.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS00615; C_TYPE_LECTIN_1; 1.
DR PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
KW Signal.
FT SIGNAL 1 23 POTENTIAL.
SQ CHAIN 24 152 HALYXIN A-CHAIN.
SQ SEQUENCE 152 AA; 17455 MW; BDD74D1DC280C28D CRC64;

Query Match 73.1%; Score 79; DB 13; Length 152;
Best Local Similarity 76.5%; Pred. No. 0.00021;
Matches 13; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 DCPSEWSSYEGFCYKPF 17
||| ||||| |||||
Db 24 DCPSEWSSYEGHCYNIF 40

Search completed: December 8, 2003, 09:54:48
Job time : 8.25714 secs

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GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: December 8, 2003, 13:34:19 ; Search time 440.543 Seconds
(without alignments)
937.879 Million cell updates/sec

Title: US-09-938-114-4
Perfect score: 108
Sequence: 1 DCPSEWSYEGFCYKPF 17

Scoring table: BLOSUM62
Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+p2n.model -DEV=xlh
-Q=/cgn2_1/USPTO.spool/US0938114/runat_08122003_091000_22859/app_query.fasta_1.725
-DB=EST -QFMT=fastap -SUFFIX=rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCLMIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEADSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US0938114 @CGN 1.1 4382 @runat_08122003_091000_22859 -NCPU=6 -ICPU=3
-NO MAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

EST :

1: em estba:*
2: em esthum:*
3: em estin:*
4: em estmu:*
5: em estov:*
6: em estpl:*
7: em estro:*
8: em htc:*
9: gb est1:*
10: gb est2:*
11: gb htc:*
12: gb est3:*
13: gb est4:*
14: gb est5:*
15: em estfun:*
16: em estom:*
17: em gss_hum:*
18: em gss_inv:*
19: em gss_pln:*
20: em gss_vrt:*
21: em gss_fun:*
22: em gss_mam:*
23: em gss_mus:*
24: em gss_pro:*
25: em gss_rod:*
26: em gss_phg:*
27: em_gss_vrl:*
28: gb_gss1:*

29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	83	76.9	172	12	BM401696 PH1A01F S
2	83	76.9	343	12	BM401656 PH1E04F S
3	83	76.9	378	12	BM401618 J11C07F S
4	83	76.9	391	12	BM401469 J11B09F S
5	83	76.9	475	12	BM401621 J11D02F S
6	83	76.9	504	12	BM401628 J11E12F S
7	83	76.9	510	12	BM401667 J12H07F S
8	83	76.9	512	12	BM401495 J12B09F S
9	82	75.9	374	12	BM401520 J12G02F S
10	82	75.9	497	12	BM401552 J13E12F S
11	80	74.1	378	12	BM401620 J11C11F S
12	80	74.1	460	12	BM401460 J11D06F S
13	80	74.1	574	12	BM401417 GH061F Sn
14	80	74.1	654	12	BM401401 GH025F Sn
15	76	70.4	633	12	BM401686 PH015FB S
16	67	62.0	184	12	BM401646 J12A05F S
17	66	61.1	298	12	BM401455 J11C07F S
18	66	61.1	307	12	BM401567 J14A07F S
19	66	61.1	315	12	BM401503 J12D02F S
20	66	61.1	321	12	BM401611 J11B01F S
21	66	61.1	388	12	BM401625 J11E05F S
22	66	61.1	401	12	BM401610 J11A11F S
23	66	61.1	405	12	BM401607 J14H07F S
24	66	61.1	410	12	BM401605 J14H07F S
25	66	61.1	440	12	BM401459 J11D05F S
26	66	61.1	440	12	BM401637 J11G11F S
27	66	61.1	453	12	BM401653 J12D01F S
28	66	61.1	458	12	BM401641 J11H06F S
29	66	61.1	501	12	BM401648 J12B03F S
30	66	61.1	511	12	BM401631 J11F11F S
31	66	61.1	556	12	BM401668 J12H08F S
32	65	60.2	200	12	BM401669 J12H09F S
33	65	60.2	365	12	BM401665 J12H01F S
34	65	60.2	456	12	BM401659 J12F01F S
35	62	57.4	318	9	AI724077 RH1Z1 26
36	62	57.4	522	9	AI724149 RH1Z1 7 E
37	62	57.4	533	13	BQ656090 PRC1061 S
38	62	57.4	533	13	BQ656093 PRC1065 S
39	61	56.5	556	9	AA618477 mm09a06.s
40	61	56.5	589	10	AW945357 PM3-EN000
41	61	56.5	595	10	BE825502 PM3-EN000
42	61	56.5	598	13	BU323232 603490804
43	61	56.5	702	13	BU266055 603815327
44	61	56.5	703	13	BU269611 603816223
45	61	56.5	726	13	BU230613 603399651

ALIGNMENTS

RESULT 1
BM401696 172 bp mRNA linear EST 01-MAY-2002
LOCUS PH1A01F Snake Bothrops insularis library IL2 Bothrops insularis
DEFINITION cDNA 5' similar to Snake venom C-type lectin, mRNA sequence.
ACCESSION BM401696
VERSION BM401696.1 GI:20376324
KEYWORDS EST.
SOURCE Bothrops insularis (island jararaca)
ORGANISM Bothrops insularis
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
Viperidae; Crotalinae; Bothrops.

12459276
 Contact: Paulo Lee Ho
 Centro de Biotecnologia
 Instituto Butantan
 Av. Vital Brazil, 1500, Sao Paulo SP, BRAZIL, 05503-900
 Tel: 55 11 37 26 7222 ext. 2083
 Fax: 55 11 37 26 1505
 Email: hoplee@usp.br
 This EST corresponds to cluster BITL01A (see Reference)
 Seg primer: Mt3F.

BASE COUNT

79 a	--83 c	90 g	86 t	5 others
------	--------	------	------	----------

/clone lib="Snake Bothrops insularis library IL3"
Note="Organ: venom glands; Vector: pGEM11zf+; Site 1: Eco
RI; Site 2: Not I; Sug of mRNA from Bothrops insularis
venom glands were primed with oligo- (dT) and reverse
transcribed to cDNA using Superscript Plasmid System for
cDNA Synthesis and Cloning (LifeTechnologies). The cDNAs
were selected by size (350-600 pb and up 600 pb) in
agarose gel electrophoresis, linked to Eco RI adapters and
directionally cloned in pGEM11zf+ vector (Promega). ESTs
were generated from random clones and grouped in unique
sequences. The putative identification of each EST or
cluster was obtained through Blast searches (e-value <
e-05)."

DB:	12	Gaps:	0
US-09-938-114-4 (1-17) x BM401656 (1-343)			

LOCUS BM401618 378 bp mRNA linear EST 01-MAY-2002
DEFINITION J1LC07F Snake Bothrops insularis library IL3 Bothrops insularis
CDNA 5' similar to Snake venom C-type lectin, mRNA sequence.

REFERENCE AUTHORS TITLE	JOURNAL MEDLINE PUBMED	COMMENT
Viperidae; Crotalinae; Bothrops. 1 (bases 1 to 378)		
Junqueira-de-Azevedo, I.L.M. and Ho, P.L. A survey of gene expression and diversity in the venom glands of the pitviper snake Bothrops insularis through the generation of expressed sequence tags (ESTs)	Gene 239 (1-2), 279-291 (2002) 22347338	
	12459276	
Contact: Paulo Lee Ho		
Centro de Biotecnologia		
Instituto Butantan		
Av. Vital Brazil, 1500, Sao Paulo SP, BRAZIL, 05503-900		
Tel: 55 11 37 26 7222 ext. 2083		
Fax: 55 11 37 26 1505		

Email: hoplee@usp.br
This EST corresponds to cluster BITL01A (see Reference)
Seq primer: M13F.
Location/Qualifiers

FEATURES

source
1..378
/organism="Bothrops insularis"
/mol_type="mRNA"
/db_xref="taxon:8723"

/tissue_type="venom glands"
/clone_lib="Snake Bothrops insularis library IL3"
/note="Organ: venom glands; Vector: pGEM11zf+; Site 1: Eco RI; Site 2: Not I; Sug of mRNA from Bothrops insularis venom glands were primed with oligo-(dT) and reverse transcribed to cDNA using Superscript Plasmid System for cDNA Synthesis and Cloning (Life Technologies). The cDNAs were selected by size (350-600 pb and up 600 pb) in agarose gel electrophoresis, linked to Eco RI adapters and directionally cloned in pGEM11zf+ vector (Promega). ESTs were generated from random clones and grouped in unique sequences. The putative identification of each EST or cluster was obtained through Blast searches (e-value < e-05)."

BASE COUNT 88 a 91 c 102 g 95 t 2 others

ORIGIN

Alignment Scores:
Pred. No.: 0.00967 Length: 378
Score: 83.00 Matches: 13
Percent Similarity: 82.35% Conservative: 1
Best Local Similarity: 76.47% Mismatches: 3
Query Match: 76.85% Indels: 0
DB: 12 Gaps: 0

US-09-938-114-4 (1-17) x BM401618 (1-378)

Qy 1 AspCysProSerGluTrpSerSerTyrGluGlyPheCysTyrLysProPhe 17
Db 78 GATTGTCCTCTGATTGTCCTATGAGGCGATTGCTACAGCTCTTC 128

RESULT 4

BM401469 391 bp mRNA linear EST 01-MAY-2002
LOCUS JH1E09F Snake Bothrops insularis library IL3 Bothrops insularis
DEFINITION cDNA 5' similar to Snake venom C-type lectin, mRNA sequence.

ACCSSION BM401469
VERSION BM401469.1 GI:20376097

KEYWORDS

SOURCE Bothrops insularis (island jararaca)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea; Viperidae; Crotalinae; Bothrops.

REFERENCE

AUTHORS Junqueira-de-Azevedo, I.L.M. and Ho, P.L.

TITLE A survey of gene expression and diversity in the venom glands of the pitviper snake Bothrops insularis through the generation of expressed sequence tags (ESTs)

JOURNAL Gene 299 (1-2), 279-291 (2002)

MEDLINE

22347338

PUBMED

12459276

COMMENT Contact: Paulo Lee Ho

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Email: hoplee@usp.br

This EST corresponds to cluster BITL03A (see Reference)

Seq primer: M13F.

FEATURES

source Location/Qualifiers

1..391

/organism="Bothrops insularis"

/mol_type="mRNA"

/db_xref="taxon:8723"

/tissue_type="venom glands"

/clone_lib="Snake Bothrops insularis library IL3"

/note="Organ: venom glands; Vector: pGEM11zf+; Site 1: Eco RI; Site 2: Not I; Sug of mRNA from Bothrops insularis venom glands were primed with oligo-(dT) and reverse transcribed to cDNA using Superscript Plasmid System for

cDNA Synthesis and Cloning (Life Technologies). The cDNAs were selected by size (350-600 pb and up 600 pb) in agarose gel electrophoresis, linked to Eco RI adapters and directionally cloned in pGEM11zf+ vector (Promega). ESTs were generated from random clones and grouped in unique sequences. The putative identification of each EST or cluster was obtained through Blast searches (e-value < e-05)."

BASE COUNT 91 a 92 c 113 g 95 t

ORIGIN

Alignment Scores:
Pred. No.: 0.0101 Length: 391
Score: 83.00 Matches: 13
Percent Similarity: 82.35% Conservative: 1
Best Local Similarity: 76.47% Mismatches: 3
Query Match: 76.85% Indels: 0
DB: 12 Gaps: 0

US-09-938-114-4 (1-17) x BM401469 (1-391)

Qy 1 AspCysProSerGluTrpSerSerTyrGluGlyPheCysTyrLysProPhe 17
Db 135 GATTGTCCTCTGATTGTCCTATGAGGCGATTGCTACAGCTCTTC 185

RESULT 5

BM401621

LOCUS

JH1D02F Snake Bothrops insularis library IL3 Bothrops insularis
DEFINITION cDNA 5' similar to Snake venom C-type lectin, mRNA sequence.

ACCSSION BM401621

VERSION BM401621.1 GI:20376249

KEYWORDS

SOURCE Bothrops insularis (island jararaca)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea; Viperidae; Crotalinae; Bothrops.

REFERENCE

AUTHORS Junqueira-de-Azevedo, I.L.M. and Ho, P.L.

TITLE A survey of gene expression and diversity in the venom glands of the pitviper snake Bothrops insularis through the generation of expressed sequence tags (ESTs)

JOURNAL Gene 299 (1-2), 279-291 (2002)

MEDLINE

22347338

PUBMED

12459276

COMMENT Contact: Paulo Lee Ho

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Tel: 55 11 37 26 7222 ext. 2083

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Email: hoplee@usp.br

This EST corresponds to cluster BITL01A (see Reference)

Seq primer: M13F.

FEATURES

source Location/Qualifiers

1..475

/organism="Bothrops insularis"

/mol_type="mRNA"

/db_xref="taxon:8723"

/tissue_type="venom glands"

/clone_lib="Snake Bothrops insularis library IL3"

/note="Organ: venom glands; Vector: pGEM11zf+; Site 1: Eco RI; Site 2: Not I; Sug of mRNA from Bothrops insularis venom glands were primed with oligo-(dT) and reverse transcribed to cDNA using Superscript Plasmid System for

cDNA Synthesis and Cloning (LifeTechnologies). The cDNAs were selected by size (350-600 pb and up 600 pb) in agarose gel electrophoresis, linked to Eco RI adapters and directionally cloned in pGEM11zf+ vector (Promega). ESTs were generated from random clones and grouped in unique sequences. The putative identification of each EST or cluster was obtained through Blast searches (e-value < e-05).

BASE COUNT 113 a 111 c 133 g 117 t 1 others
ORIGIN

Alignment Scores:
Pred. No.: 0.0133 Length: 475
Score: 83.00 Matches: 13
Percent Similarity: 82.35% Conservative: 1
Best Local Similarity: 76.47% Mismatches: 3
Query Match: 76.85% Indels: 0
DB: 12 Gaps: 0

US-09-938-114-4 (1-17) x BM401621 (1-475)

Qy 1 AspCysProSerGluTrpSerSerTyrGluGlyPheCysTyrLysProphe 17
|||||
Db 129 GATTGTCCTGCTGATTGTCCTGATGAGGCGATTGCTACAGCTCTTC 179

RESULT 6

BM401628

LOCUS BM401628 504 bp mRNA linear EST 01-MAY-2002
DEFINITION JLI12F Snake Bothrops insularis library IL3 Bothrops insularis
cDNA 5' similar to Snake venom C-type lectin, mRNA sequence.

ACCESSION BM401628

VERSION BM401628.1 GI:20376256

KEYWORDS EST.

SOURCE Bothrops insularis (island jararaca)

ORGANISM Bothrops insularis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
Viperidae; Crotalinae; Bothrops.

REFERENCE 1 (bases 1 to 504)

A survey of gene expression and diversity in the venom glands of the pitviper snake Bothrops insularis through the generation of expressed sequence tags (ESTs)

Gene 299 (1-2), 279-291 (2002)

22347338

PUBMED 12459276

COMMENT Contact: Paulo Lee Ho

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Fax: 55 11 37 26 1505

Email: hoplee@usp.br

This EST corresponds to cluster BITL01A (see Reference)

Seq primer: M13F.

FEATURES

source

1..504

Location/Qualifiers

/organism="Bothrops insularis"

/mol_type="mRNA"

/db_xref="taxon:8723"

/tissue type="venom glands"

/clone lib="Snake Bothrops insularis library IL3"
RI; Site 2; Not 1; 5ug of mRNA from Bothrops insularis
venom glands were primed with oligo-(dT) and reverse
transcribed to cDNA using Superscript Plasmid System for
cDNA Synthesis and Cloning (LifeTechnologies). The cDNAs

were selected by size (350-600 pb and up 600 pb) in
agarose gel electrophoresis, linked to Eco RI adapters and
directionally cloned in pGEM11zf+ vector (Promega). ESTs

were generated from random clones and grouped in unique
sequences. The putative identification of each EST or
cluster was obtained through Blast searches (e-value <

e-05)."
BASE COUNT 128 a 113 c 140 g 120 t 3 others
ORIGIN

Alignment Scores:

Pred. No.: 0.0144 Length: 504
Score: 83.00 Matches: 13
Percent Similarity: 82.35% Conservative: 1
Best Local Similarity: 76.47% Mismatches: 3
Query Match: 76.85% Indels: 0
DB: 12 Gaps: 0

US-09-938-114-4 (1-17) x BM401628 (1-504)

Qy 1 AspCysProSerGluTrpSerSerTyrGluGlyPheCysTyrLysProphe 17
|||||
Db 96 GATTGTCCTGCTGATTGTCCTGATGAGGCGATTGCTACAGCTCTTC 146

RESULT 7

BM401667

LOCUS BM401667 510 bp mRNA linear EST 01-MAY-2002
DEFINITION JLI2H07F Snake Bothrops insularis library IL3 Bothrops insularis
cDNA 5' similar to Snake venom C-type lectin, mRNA sequence.

ACCESSION BM401667

VERSION BM401667.1 GI:20376295

KEYWORDS EST.

SOURCE Bothrops insularis (island jararaca)

ORGANISM Bothrops insularis

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
Viperidae; Crotalinae; Bothrops.

REFERENCE 1 (bases 1 to 510)

A survey of gene expression and diversity in the venom glands of the pitviper snake Bothrops insularis through the generation of expressed sequence tags (ESTs)

Gene 299 (1-2), 279-291 (2002)

22347338

PUBMED 12459276

COMMENT Contact: Paulo Lee Ho

Centro de Biotecnologia

Instituto Butantan

Av. Vital Brazil, 1500, Sao Paulo SP, BRAZIL, 05503-900

Tel: 55 11 37 26 7222 ext. 2083

Fax: 55 11 37 26 1505

Email: hoplee@usp.br

This EST corresponds to cluster BITL01A (see Reference)

Seq primer: M13F.

FEATURES

source

1..510

Location/Qualifiers

/organism="Bothrops insularis"

/mol_type="mRNA"

/db_xref="taxon:8723"

/tissue type="venom glands"

/clone lib="Snake Bothrops insularis library IL3"
RI; Site 2; Not 1; 5ug of mRNA from Bothrops insularis
venom glands were primed with oligo-(dT) and reverse
transcribed to cDNA using Superscript Plasmid System for
cDNA Synthesis and Cloning (LifeTechnologies). The cDNAs

were selected by size (350-600 pb and up 600 pb) in
agarose gel electrophoresis, linked to Eco RI adapters and
directionally cloned in pGEM11zf+ vector (Promega). ESTs

were generated from random clones and grouped in unique
sequences. The putative identification of each EST or
cluster was obtained through Blast searches (e-value <

e-05)."

BASE COUNT 128 a 117 c 141 g 121 t 3 others

ORIGIN

Alignment Scores:

Pred. No.: 0.0146 Length: 510
Score: 83.00 Matches: 13

Percent Similarity: 82.35% Conservative: 1
 Best Local Similarity: 76.47% Mismatches: 3
 Query Match: 76.85% Indels: 0
 DB: 12 Gaps: 0

US-09-938-114-4 (1-17) x BM401667 (1-510)

QY 1 AspCysProSerGluTrpSerSerTyrGluGlyPheCysTyrIlysProPhe 17
 DB 93 GATTGTCCTCTGATTGGTCCCTATGAAGGCGATTGCTACAAGCTCTTC 143

RESULT 8

BM401495
 LOCUS BM401495 512 bp mRNA linear EST 01-MAY-2002
 DEFINITION JH2809F Snake Bothrops insularis library IL3 Bothrops insularis
 cDNA 5' similar to Snake venom C-type lectin, mRNA sequence.
 ACCESSION BM401495
 VERSION BM401495.1 GI:20376123
 KEYWORDS EST.
 SOURCE Bothrops insularis (island jararaca)
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
 Viperidae; Crotalinae; Bothrops.

REFERENCE

1 (bases 1 to 512)
 Junqueira-de-Azevedo, I.L.M. and Ho, P.L.
 A survey of gene expression and diversity in the venom glands of
 the pitviper snake Bothrops insularis through the generation of
 expressed sequence tags (ESTs)
 Gene 299 (1-2), 279-291 (2002)
 MEDLINE 22347338
 PUBMED 12459276

COMMENT

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 Instituto Butantan
 Av. Vital Brazil, 1500, Sao Paulo SP, BRAZIL, 05503-900
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 Fax: 55 11 37 26 1505
 Email: hoplee@usp.br
 This EST corresponds to cluster BITL01A (see Reference)
 Seq primer: M13F.

FEATURES

Location/Qualifiers
 1..512
 /organism="Bothrops insularis"
 /mol_type="mRNA"
 /db_xref="taxon:8723"
 /tissue type="venom glands"
 /clone_lib="Snake Bothrops insularis library IL3"
 /note="Organ: venom glands; Vector: pGEM11zf+; Site 1: Eco
 RI; Site 2: Not I; Sug of mRNA from Bothrops insularis
 venom glands were primed with oligo-(dT) and reverse
 transcribed to cDNA using Superscript plasmid system for
 cDNA Synthesis and Cloning (Life Technologies). The cDNAs
 were selected by size (350-600 pb and up 600 pb) in
 agarose gel electrophoresis, linked to Eco RI adapters and
 directionally cloned in pGEM11zf+ vector (Promega). ESTs
 were generated from random clones and grouped in unique
 sequences. The putative identification of each EST or
 cluster was obtained through Blast searches (e-value <
 e-05)."
 BASE COUNT 129 a 116 c 143 g 119 t 5 others
 ORIGIN

Alignment Scores:

Pred. No.: 0.0147 Length: 512
 Score: 83.00 Matches: 13
 Percent Similarity: 82.35% Conservative: 1
 Best Local Similarity: 76.47% Mismatches: 3
 Query Match: 76.85% Indels: 0
 DB: 12 Gaps: 0

US-09-938-114-4 (1-17) x BM401495 (1-512)

QY
 DB

RESULT 9

BM401520
 LOCUS BM401520 374 bp mRNA linear EST 01-MAY-2002
 DEFINITION JH2802F Snake Bothrops insularis library IL3 Bothrops insularis
 cDNA 5' similar to Snake venom C-type lectin, mRNA sequence.
 ACCESSION BM401520
 VERSION BM401520.1 GI:20376148
 KEYWORDS EST.
 SOURCE Bothrops insularis (island jararaca)
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
 Viperidae; Crotalinae; Bothrops.

REFERENCE

1 (bases 1 to 374)
 Junqueira-de-Azevedo, I.L.M. and Ho, P.L.
 A survey of gene expression and diversity in the venom glands of
 the pitviper snake Bothrops insularis through the generation of
 expressed sequence tags (ESTs)
 Gene 299 (1-2), 279-291 (2002)
 MEDLINE 22347338
 PUBMED 12459276

COMMENT

Contact: Paulo Lee Ho
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 Av. Vital Brazil, 1500, Sao Paulo SP, BRAZIL, 05503-900
 Tel: 55 11 37 26 7222 ext. 2083
 Fax: 55 11 37 26 1505
 Email: hoplee@usp.br
 This EST corresponds to cluster BITL06A (see Reference)
 Seq primer: M13F.

FEATURES

Location/Qualifiers
 1..374
 /organism="Bothrops insularis"
 /mol_type="mRNA"
 /db_xref="taxon:8723"
 /tissue type="venom glands"
 /clone_lib="Snake Bothrops insularis library IL3"
 /note="Organ: venom glands; Vector: pGEM11zf+; Site 1: Eco
 RI; Site 2: Not I; Sug of mRNA from Bothrops insularis
 venom glands were primed with oligo-(dT) and reverse
 transcribed to cDNA using Superscript plasmid system for
 cDNA Synthesis and Cloning (Life Technologies). The cDNAs
 were selected by size (350-600 pb and up 600 pb) in
 agarose gel electrophoresis, linked to Eco RI adapters and
 directionally cloned in pGEM11zf+ vector (Promega). ESTs
 were generated from random clones and grouped in unique
 sequences. The putative identification of each EST or
 cluster was obtained through Blast searches (e-value <
 e-05)."
 BASE COUNT 83 a 83 c 114 g 94 t
 ORIGIN

Alignment Scores:

Pred. No.: 0.0135 Length: 374
 Score: 82.00 Matches: 13
 Percent Similarity: 82.35% Conservative: 1
 Best Local Similarity: 76.47% Mismatches: 3
 Query Match: 75.93% Indels: 0
 DB: 12 Gaps: 0

US-09-938-114-4 (1-17) x BM401520 (1-374)

QY 1 AspCysProSerGluTrpSerSerTyrGluGlyPheCysTyrIlysProPhe 17
 DB 130 GATTGTCCTCTGATTGGTCCCTATGAAGGCGATTGCTACAAGCTCTTC 180

RESULT 10

BM401552
 LOCUS BM401552 497 bp mRNA linear EST 01-MAY-2002

JOURNAL
MEDLINE
PUBMED
COMMENT

expressed sequence tags (ESTs)
Gene 299 (1-2), 279-291 (2002)
22347338
12459276
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Tel: 55 11 37 26 7222 ext. 2083
Fax: 55 11 37 26 1505
Email: hoplee@usp.br
This EST corresponds to cluster BITL13A (see Reference)
Seq primer: M13F.

FEATURES

source
Location/Qualifiers

1..460
/organism="Bothrops insularis"
/mol_type="mRNA"
/db_xref="taxon:8723"
/tissue_type="venom glands"
/clone_lib="Snake Bothrops insularis library IL3"
/notes="Organ: venom glands; Vector: pGEM11zf+; Site 1: Eco RI; Site 2: Not I; Sug of mRNA from Bothrops insularis venom glands were primed with oligo-(dT) and reverse transcribed to cDNA using Superscript Plasmid System for cDNA Synthesis and Cloning (Life Technologies). The cDNAs were selected by size (350-600 pb and up 600 pb) in agarose gel electrophoresis, linked to Eco RI adapters and directionally cloned in pGEM11zf+ vector (Promega). ESTs were generated from random clones and grouped in unique sequences. The putative identification of each EST or cluster was obtained through Blast searches (e-value < e-05)."

BASE COUNT 106 a 106 c 145 g 103 t
ORIGIN

Alignment Scores:
Pred. No.: 0.0361 Length: 460
Score: 80.00 Matches: 12
Percent Similarity: 82.35% Conservative: 2
Best Local Similarity: 70.59% Mismatches: 3
Query Match: 74.07% Indels: 0
DB: 12 Gaps: 0

US-09-938-114-4 (1-17) x BM401460 (1-460)

QY 1 AspCysProSerGluTrpSerTyrGluGlyPheCysTyrIysProPhe 17
143 GATTGTCCTGATGGTCTCTCTATGAGGAGGATTGCTACAGGGCTTC 193

RESULT 13

BM401417

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

COMMENT

BM401417 574 bp mRNA linear EST 01-MAY-2002
GH061F Snake Bothrops insularis library IL2 Bothrops insularis cDNA
5' similar to Snake venom C-type lectin, mRNA sequence.
BM401417
BM401417.1 GI:20376045
EST.
Bothrops insularis (island jararaca)
Bothrops insularis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
Viperidae; Crotalinae; Bothrops.
1 (bases 1 to 574)
Junqueira-de-Azevedo, I.L.M. and Ho, P.L.
A survey of gene expression and diversity in the venom glands of the pitviper snake Bothrops insularis through the generation of expressed sequence tags (ESTs)
Gene 299 (1-2), 279-291 (2002)
12459276
Contact: Paulo Lee Ho
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Tel: 55 11 37 26 7222 ext. 2083
Fax: 55 11 37 26 1505
Email: hoplee@usp.br
This EST corresponds to cluster BITL10A (see Reference)
Seq primer: M13F.

FEATURES

source
Location/Qualifiers

1..574
/organism="Bothrops insularis"
/mol_type="mRNA"
/db_xref="taxon:8723"
/tissue_type="venom glands"
/clone_lib="Snake Bothrops insularis library IL2"
/notes="Organ: venom glands; Vector: pGEM11zf+; Site 1: Eco RI; Site 2: Not I; Sug of mRNA from Bothrops insularis venom glands were primed with oligo-(dT) and reverse transcribed to cDNA using Superscript Plasmid System for cDNA Synthesis and Cloning (Life Technologies). The cDNAs were selected by size (350-600 pb and up 600 pb) in agarose gel electrophoresis, linked to Eco RI adapters and directionally cloned in pGEM11zf+ vector (Promega). ESTs were generated from random clones and grouped in unique sequences. The putative identification of each EST or cluster was obtained through Blast searches (e-value < e-05)."

BASE COUNT 146 a 129 c 161 g 134 t 4 others
ORIGIN

Alignment Scores:
Pred. No.: 0.049 Length: 574
Score: 80.00 Matches: 12
Percent Similarity: 82.35% Conservative: 2
Best Local Similarity: 70.59% Mismatches: 3
Query Match: 74.07% Indels: 0
DB: 12 Gaps: 0

US-09-938-114-4 (1-17) x BM401417 (1-574)

QY 1 AspCysProSerGluTrpSerTyrGluGlyPheCysTyrIysProPhe 17
143 GATTGTCCTGATGGTCTCTCTATGAGGAGGATTGCTACAGGGCTTC 193

RESULT 14

BM401401

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

COMMENT

BM401401 654 bp mRNA linear EST 01-MAY-2002
GH025F Snake Bothrops insularis library IL2 Bothrops insularis cDNA
5' similar to Snake venom C-type lectin, mRNA sequence.
BM401401
BM401401.1 GI:20376029
EST.
Bothrops insularis (island jararaca)
Bothrops insularis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
Viperidae; Crotalinae; Bothrops.
1 (bases 1 to 654)
Junqueira-de-Azevedo, I.L.M. and Ho, P.L.
A survey of gene expression and diversity in the venom glands of the pitviper snake Bothrops insularis through the generation of expressed sequence tags (ESTs)
Gene 299 (1-2), 279-291 (2002)
12459276
Contact: Paulo Lee Ho
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Tel: 55 11 37 26 7222 ext. 2083
Fax: 55 11 37 26 1505
Email: hoplee@usp.br
This EST corresponds to cluster BITL10A (see Reference)
Seq primer: M13F.

FEATURES

Location/Qualifiers

```

source
1. .654
/organism="Bothrops insularis"
/mol_type="mRNA"
/db_xref="taxon:8723"
/tissue_type="venom glands"
/clone_lib="Snake Bothrops insularis library IL2"
/note="Organ: venom glands; Vector: pGEM11zf+; Site:1: Eco
RI; Site:2: Not I; Sug of mRNA from Bothrops insularis
venom glands were primed with oligo-(dT) and reverse
transcribed to cDNA using Superscript Plasmid System for
cDNA Synthesis and Cloning (Life Technologies). The cDNAs
were selected by size (350-600 pb and up 600 pb) in
agarose gel electrophoresis, linked to Eco RI adapters and
directionally cloned in pGEM11zf+ vector (Promega). ESTs
were generated from random clones and grouped in unique
sequences. The putative identification of each EST or
cluster was obtained through Blast searches (e-value <
e-05)."
```

BASE COUNT 154 a 156 c 175 g 161 t 8 others

ORIGIN

Alignment Scores:

Pred. No.:	Score:	Length:
0.0587	80.00	654
Percent Similarity:	82.35%	Matches: 12
Best Local Similarity:	70.59%	Conservative: 2
Query Match:	74.07%	Mismatches: 3
DB:	12	Indels: 0
		Gaps: 0

US-09-938-114-4 (1-17) x BM401401 (1-654)

QY 1 AspCysProSerGluTrpSerSerTyrGluGlyPheCysTyrLysProphe 17
|||||CCCCCTGATGGTCTCTCTCTGAGGGAGTGTCTACAGGGCTTTC 193

Db 143 GATTGTCCTCTGATGGTCTCTCTCTGAGGGAGTGTCTACAGGGCTTTC 193

RESULT 15

BM401686

LOCUS PH015FB Snake Bothrops insularis library IL2 Bothrops insularis

DEFINITION cDNA 5' similar to Snake venom C-type lectin, mRNA sequence.

ACCESSION BM401686

VERSION BM401686.1 GI:20376314

KEYWORDS EST.

SOURCE Bothrops insularis (island jararaca)

ORGANISM Bothrops insularis

REFERENCE 1 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea; Viperidae; Crotalinae; Bothrops.

AUTHORS Junqueira-de-Azevedo, I.L.M. and Ho, P.L.

TITLE A survey of gene expression and diversity in the venom glands of the pitviper snake Bothrops insularis through the generation of expressed sequence tags (ESTs)

JOURNAL Gene 299 (1-2), 279-291 (2002)

MEDLINE 22347338

PUBMED 12459276

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Fax: 55 11 37 26 1505
Email: hoplee@usp.br
This EST corresponds to cluster BITL02A (see Reference)
Seq primer: M13F.

FEATURES

source

1. .633

/organism="Bothrops insularis"

/mol_type="mRNA"

/db_xref="taxon:8723"

/tissue_type="venom glands"

/clone_lib="Snake Bothrops insularis library IL2"

/note="Organ: venom glands; Vector: pGEM11zf+; Site:1: Eco

RI; Site:2: Not I; Sug of mRNA from Bothrops insularis venom glands were primed with oligo-(dT) and reverse transcribed to cDNA using Superscript Plasmid System for cDNA Synthesis and Cloning (Life Technologies). The cDNAs were selected by size (350-600 pb and up 600 pb) in agarose gel electrophoresis, linked to Eco RI adapters and directionally cloned in pGEM11zf+ vector (Promega). ESTs were generated from random clones and grouped in unique sequences. The putative identification of each EST or cluster was obtained through Blast searches (e-value < e-05)."

BASE COUNT 145 a 148 c 155 g 171 t 14 others

ORIGIN

Alignment Scores:

Pred. No.:	Score:	Length:
0.226	76.00	633
Percent Similarity:	76.47%	Matches: 12
Best Local Similarity:	70.59%	Conservative: 1
Query Match:	70.37%	Mismatches: 4
DB:	12	Indels: 0
		Gaps: 0

US-09-938-114-4 (1-17) x BM401686 (1-633)

QY 1 AspCysProSerGluTrpSerSerTyrGluGlyPheCysTyrLysProphe 17
|||||CCCCCTGATGGTCTCTCTCTGAGGGAGTGTCTACAGGGCTTTC 132

Db 82 GATTGTCCTCTGATGGTCTCTCTCTGAGGGAGTGTCTACAGGGCTTTC 132

Search completed: December 8, 2003, 17:24:34

Job time : 441.543 secs